

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hadlaczky, Gyula
Szalay, Aladar
- (ii) TITLE OF THE INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Heller Ehrman White & McAuliffe
(B) STREET: 4250 Executive Square, 7th Floor
(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 28-NOV-2000
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/835,682
(B) FILING DATE: 10-APR-1997
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/695,191
(B) FILING DATE: 07-AUG-1996
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/682,080
(B) FILING DATE: 15-JUL-1996
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/629,822
(B) FILING DATE: 10-APR-1996
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Seidman, Stephanie L
(B) REGISTRATION NUMBER: 33,779
(C) REFERENCE/DOCKET NUMBER: 6869-402E
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 858-450-8403
(B) TELEFAX: 858-587-5360
(C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:
 (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | |
|------------|-------------|------------|-------------|------------|------------|------|
| GAATTCATCA | TTTTTCANGT | CCTCAAGTGG | ATGTTTCTCA | TTNCCATGA | TTTAAAGTTT | 60 |
| TCTCGCCATA | TTCTGGTCC | TACAGTGTGC | ATTTCTCCAT | TTNCACGTT | TTNCAGTGAT | 120 |
| TTCGTCATTT | TCAAGTCCTC | AAGTGGATGT | TTCTCATTTN | CCATGAATT | CAGTTTTCTN | 180 |
| GCCATATTCC | ACGTCCTACA | GNGGACATTT | CTAAATTTNC | CACCTTTTTT | AGTTTTCTCT | 240 |
| GCCATATTTT | ACGTCCTAAA | ATGTGTATTT | CTCGTTTNCC | GTGATTTTCA | GTTTTCTCGC | 300 |
| CAGATTCAG | GTCCTATAAT | GTGCATTTCT | CATTTNNCAC | GTTTTTCAGT | GATTTCTGTC | 360 |
| TTTTTTCAAG | TCGGCAAGTG | GATGTTTCTC | ATTTNCCATG | ATTTNCAGTT | TTCTTGNAAT | 420 |
| ATTCCATGTC | CTACAATGAT | CATTTTAAAT | TTTCCACCTT | TTTCAATTTT | CACGCCATAT | 480 |
| TTCATGTCCT | AAAGTGTATA | TTTCTCCTTT | TCCGCGATTT | TCAGTTTCT | CGCCATATTC | 540 |
| CAGGTCCTAC | AGTGTGCATT | CCTCATTTTT | CACCTTTTTT | ACTGATTTCT | TCATTTTCA | 600 |
| AGTCGTCAAC | TGGATCTTTC | TAATTTTCCA | TGATTTTTCAG | TTATCTTGTC | ATATTCATG | 660 |
| TCCTACAGTG | GACATTTCTA | AATTTTCCAA | CTTTTCAAT | TTTTCTCGAC | ATATTGACG | 720 |
| TGCTAAAGTG | TGTATTTCTT | ATTTTCCGTG | ATTTTCAGTT | TTCTCGCCAT | ATTCCAGGTC | 780 |
| CTAATAGTGT | GCATTTCTCA | TTTTTCACGT | TTTTTCAGTG | TTTCGTCAT | TTTCCAGTT | 840 |
| GTCAAGGGGA | TGTTTCTCAT | TTTCCATGAG | TGTCAGTTTT | CTTGCTATAT | TCCATGTCTT | 900 |
| ACAGTGACAT | TTCTAAATAT | TATACCTTTT | TCAGTTTTTC | TCACCATATT | TCACGTCCTA | 960 |
| AAGTATATAT | TTCTCATTTT | CCCTGATTTT | CAGTTTCTTT | GCCATATTCC | AGGTCCTACA | 1020 |
| GTGTGCATTT | CTCATTTTTC | ACGTTTTTCA | GTAATTTCTT | CATTTTAA | GCCCTCAAAT | 1080 |
| GGATGTTTCT | CATTTTCCAT | GATTTTCAGT | TTTCTTGCCA | TATACCATGT | CCTACAGTGG | 1140 |
| ACATTTCTAA | ATTATCCACC | TTTTTCAGTT | TTTCATCGGC | ACATTTACAG | TCCTAAAGTG | 1200 |
| TGTATTTCTA | ATTTTCAGTG | ATTTTCAGTT | TTCTCGCCAT | ATTCCAGGAC | CTACAGTGTG | 1260 |
| CATTTCTCAT | TTTTTCACGTT | TTTCAGTGAA | TTC | | | 1293 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1044 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:
 (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AGGCCTATGG | TGAAAAAGGA | AATATCTTCC | CCTGAAAACT | AGACAGAAGG | ATTCTCAGAA | 60 |
| TCTTATTTGT | GATGTGCGCC | CCTCAACTAA | CAGTGTTGAA | GCTTTCTTTT | GATAGAGCAG | 120 |
| TTTTGAAACA | CTCTTTTGT | AAAATCTGCA | AGAGGATATT | TGGATAGCTT | TGAGGATTTT | 180 |
| CGTTGGAAC | GGGATTGTCT | TCATATAAAC | CCTAGACAGA | AGCATTCTCA | GAAGCTTCAT | 240 |
| TGGGATGTTT | CAGTTGAAGT | CACAGTGTTG | AACAGTCCCC | TTTCATAGAG | CAGGTTTGAA | 300 |
| AACTCTTTT | TTGTAGTATC | TGGAAGTGGA | CATTTGGAGC | GATCTCAGGA | CTGCGGTGAA | 360 |
| AAAGGAAATA | TCTTCCAATA | AAAGCTAGAT | AGAGGCAATG | TCAGAAACCT | TTTTCATGAT | 420 |
| GTATCTACTC | AGCTAACAGA | GTTGAACCTT | CCTTTGAGAG | AGCAGTTTGT | AAACCTTCAT | 480 |
| TTTGTGGAAT | CTGCAAGTGG | ATATTTGTCT | AGCTTTGAGG | ATTTCTGTTG | GAAACGGGAT | 540 |
| TACATATAAA | AAGCAGACAG | CAGCATTCCC | AGAACTTCT | TTGTGATGTT | TGCATTCAAG | 600 |
| TCACAGAGTT | GAACATTCCC | TTTCATAGAG | CAGGTTTGAA | ACACACTTTT | TGATGTATCT | 660 |

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|------|
| GGATGTGGAC | ATTTGCAGCG | CTTTCAGGCC | TAAGGTGAAA | AGGAAATATC | TTCCCCTGAA | 720 |
| AACTAGACAG | AAGCATTCTC | AGAAACTTAT | TTGTGATGTG | CGCCCTCAAC | TAACAGTGTT | 780 |
| GAAGCTTTCT | TTTGATAGAG | GCAGTTTTGA | AACACTCTTT | TGTGGAATCT | GCAAGTGGAT | 840 |
| ATTTGTCTAG | CTTTGAGGAT | TTCTTTGGAA | ACGGGATTAC | ATATAAAAAG | CAGACAGCAG | 900 |
| CATTCCCAGA | ATCTTGTTTG | TGATGTTTGC | ATTCAAGTCA | CAGAGTTGAA | CATTCCTTTT | 960 |
| CAGAGAGCAG | GT'TTGAACAC | TCTTTTTATA | GTATCTGGAT | GTGGACATTT | GGAGCGCTTT | 1020 |
| CAGGGGGGAT | CCTCTAGAAT | TCCT | | | | 1044 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| CTGCAGCTGG | GGGTCTCCAA | TCAGGCAGGG | CCCCCTTACT | ACTCAGATGG | GGTGGCCGAG | 60 |
| TAGGGGAAGG | GGGTGCAGGC | TGCATGAGTG | GACACAGCTG | TAGGACTACC | TGGGGGCTGT | 120 |
| GGATCTATGG | GGGTGGGGAG | AAGCCCAGTG | ACAGTGCCTA | GAAGAGACAA | GGTGGCCTGA | 180 |
| GAGGGTCTGA | GGAACATAGA | GCTGGCCATG | TTGGGGCCAG | GTCTCAAGCA | GGAAGTGAGG | 240 |
| AATGGGACAG | GCTTGAGGAT | ACTCTACTCA | GTAGCCAGGA | TAGCAAGGAG | GGCTTGGGGT | 300 |
| TGCTATCCTG | GGGTTCAACC | CCCCAGGTTG | AAGGCCCTGG | GGGAGATGGT | CCCAGGACAT | 360 |
| ATTACAATGG | ACACAGGAGG | TTGGGACACC | TGGAGTCACC | AAACAAAACC | ATGCCAAGAG | 420 |
| AGACCATGAG | TAGGGGTGTC | CAGTCCAGCC | CTCTGACTGA | GCTGCATTGT | TCAAATCCAA | 480 |
| AGGGCCCCTG | CTGCCACCTA | GTGGCTGATG | GCATCCACAT | GACCCTGGGC | CACACGCGTT | 540 |
| TAGGGTCTCT | GTGAAGACCA | AGATCCTTGT | TACATTGAAC | GACTCCTAAA | TGAGCAGAGA | 600 |
| TTTCCACCTA | TTCGAAACAA | TCACATAAAA | TCCATCCTGG | AAAAAGCCTG | GGGGATGGCA | 660 |
| CTAAGGCTAG | GGATAGGGTG | GGATGAAGAT | TATAGTTACA | GTAAGGGGTT | TAGGGTTAGG | 720 |
| GATCAACGTT | GGTTAGGAGT | TAGGGATACA | GTAGGGTACC | GGTAGGGTTA | GGGGTTAGGG | 780 |
| TTAGGGGTTA | GGGTTAGGGT | TAGGGTTAGG | GTTAGGGTTA | GGGGTTAGGG | GTTAGGGTTA | 840 |
| GGGTTAGGTT | TTGGGGTGCC | GTATTTTGGT | CTTATACGCT | GTGTTCCACT | GGCAATGAAA | 900 |
| AGAGTTCTTG | TTTTTCCTTC | AGCAATTTGT | CATTTTTTAA | AGAGTTTAGC | AATTCTAACA | 960 |
| GATATAGACC | AGCTGTGCTA | TCTCATTTGT | GTTTTCAATT | GTAACCACAT | TGTGGTTTCA | 1020 |
| ATGTGTTTAC | TTGCCATCTG | TAGATCTTCT | TTGCGTGAGG | TGTCTGTTCA | GATGTGTGTG | 1080 |
| CATTTCTTGN | NTTTNGGCTG | TTTAACTTAT | TGTTTAGTTT | TAATAATTTT | TTATATATTT | 1140 |
| GAAGACAAAT | CTTCTCAGA | TGTGTATTTG | CAAATATTTT | TTCAATATGA | GGCTTGCTTT | 1200 |
| TGTCTCTAAC | AAGGTCCTTT | CAGAGATAAC | TTAAATATAA | GAAATCCACA | CTGTCACTTC | 1260 |
| TTTTGTGTAT | ATCTACCTTT | TGTGTCATTT | GTTAAAATTC | ATTACCAAAC | CCAAAGGCAG | 1320 |
| ATAGCTTTTC | TTCTATTGTT | TCTTCTAGAA | ATTTGTATAG | TTTTGCATTT | TTAGTGTAAG | 1380 |
| GATGATTTTG | AGTGATTATT | TGTGTAAGTT | GTAAAGTTTT | CGTCTATATC | CATATCATTT | 1440 |
| CTTATGGTTT | CCAATTAATC | GTTCCTCAC | TATTTTTGGG | AAAGACACAG | GATAGTGGGC | 1500 |
| TTTGTTAGAG | TAGATAGGTA | GCTAGACATG | AACAGGAGGG | GGCCTCCTGG | AAAAGGGAAA | 1560 |
| GTCTGGGAAG | GCTCACCTGG | AGGACCACCA | AAAATTCACA | TATTAGTAGC | ATCTCTAGTG | 1620 |
| CTGGAGTGGA | TGGGCACCTG | TCAATTGTGG | GTAGGAGGGA | AAAGAGGTCC | TATGCAGAAA | 1680 |
| GAAACTCCCT | AGAACTCCTC | TGAAGATGCC | CCAATCATTC | ACTCTGCAAT | AAAAATGTCA | 1740 |
| GAATATTGCT | AGCTACATGC | TGATAAGGNN | AAAGGGGACA | TTCTTAAGTG | AAACCTGGCA | 1800 |
| CCATAAGTAC | AGATTAGGGC | AGAGAAGGAC | ATTCAAAAGA | GGCAGGCGCA | GTAGGTACAA | 1860 |
| ACGTGATCGC | TGTCAGTGTG | CCTGGGATGG | CGGGAAGGAG | GCTGGTGCCA | GAGTGGATTTC | 1920 |
| GTATTGATCA | CCACACATAT | ACCTCAACCA | ACAGTGAGGA | GGTCCCACAA | GCCTAAGTGG | 1980 |
| GGCAAGTTGG | GGAGCTAAGG | CAGTAGCAGG | AAAACCAGAC | AAAGAAAACA | GGTGGAGACT | 2040 |
| TGAGACAGAG | GCAGGAATGT | GAAGAAATCC | AAAATAAAAT | TCCCTGCACA | GGACTCTTAG | 2100 |
| GCTGTTTAAT | GCATCGTCTA | GTCCTACTCC | TCCCTATTTT | TCTACAATAA | ACTCTTTACA | 2160 |
| CTGTGTTTCT | TTTCAATGAA | GTTATCTGCC | ATCTTTGTAT | TGCCTCTTGG | TGAAAATGTT | 2220 |
| TCTTCCAAGT | TAAACAAGAA | CTGGGACATC | AGCTCTCCCC | AGTAATAGCT | CCGTTTCAGT | 2280 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| TTGAATTTAC | AGAACTGATG | GGCTTAATAA | CTGGCGCTCT | GACTTTAGTG | GTGCAGGAGG | 2340 |
| CCGTCACACC | GGGACCAAGA | GTGCCCTGCC | TAGTCCCCAT | CTGCCCCGAG | GTGGCGGCTG | 2400 |
| CCTCGACACT | GACAGCAATA | GGGTCCGGCA | GTGTCCCCAG | CTGCCAGCAG | GGGGCGTACG | 2460 |
| ACGACTACAC | TGTGAGCAAG | AGGGCCCTGC | AG | | | 2492 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | |
|------------|------------|----------|----|
| GGGGAATTCA | TTGGGATGTT | TCAGTTGA | 28 |
|------------|------------|----------|----|

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | |
|------------|------------|-----------|----|
| CGAAAGTCCC | CCCTAGGAGA | TCTTAAGGA | 29 |
|------------|------------|-----------|----|

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | |
|------------|------------|------------|------------|---------|
| CCGCTTAATA | CTCTGATGAG | TCCGTGAGGA | CGAAACGCTC | TCGCACC |
|------------|------------|------------|------------|---------|

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTTAAAT TAATTAAGCC CGGGC

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTTAAT TAATTCGGGC CCGTCGA

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (D) OTHER INFORMATION IL-2 signal sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT
 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

48

GTC ACA AAC AGT GCA CCT ACT
 Val Thr Asn Ser Ala Pro Thr

69

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 945 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...942

(D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AGC | TTA | AAG | ATG | ACT | TCG | AAA | GTT | TAT | GAT | CCA | GAA | CAA | AGG | AAA | CGG | 48 |
| Ser | Leu | Lys | Met | Thr | Ser | Lys | Val | Tyr | Asp | Pro | Glu | Gln | Arg | Lys | Arg | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| ATG | ATA | ACT | GGT | CCG | CAG | TGG | TGG | GCC | AGA | TGT | AAA | CAA | ATG | AAT | GTT | 96 |
| Met | Ile | Thr | Gly | Pro | Gln | Trp | Trp | Ala | Arg | Cys | Lys | Gln | Met | Asn | Val | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| CTT | GAT | TCA | TTT | ATT | AAT | TAT | TAT | GAT | TCA | GAA | AAA | CAT | GCA | GAA | AAT | 144 |
| Leu | Asp | Ser | Phe | Ile | Asn | Tyr | Tyr | Asp | Ser | Glu | Lys | His | Ala | Glu | Asn | |
| | | 35 | | | | 40 | | | | | | 45 | | | | |
| GCT | GTT | ATT | TTT | TTA | CAT | GGT | AAC | GCG | GCC | TCT | TCT | TAT | TTA | TGG | CGA | 192 |
| Ala | Val | Ile | Phe | Leu | His | Gly | Asn | Ala | Ala | Ser | Ser | Tyr | Leu | Trp | Arg | |
| | | 50 | | | | 55 | | | | | 60 | | | | | |
| CAT | GTT | GTG | CCA | CAT | ATT | GAG | CCA | GTA | GCG | CGG | TGT | ATT | ATA | CCA | GAT | 240 |
| His | Val | Val | Pro | His | Ile | Glu | Pro | Val | Ala | Arg | Cys | Ile | Ile | Pro | Asp | |
| 65 | | | | 70 | | | | | | 75 | | | | 80 | | |
| CTT | ATT | GGT | ATG | GGC | AAA | TCA | GGC | AAA | TCT | GGT | AAT | GGT | TCT | TAT | AGG | 288 |
| Leu | Ile | Gly | Met | Gly | Lys | Ser | Gly | Lys | Ser | Gly | Asn | Gly | Ser | Tyr | Arg | |
| | | | 85 | | | | | | 90 | | | | 95 | | | |
| TTA | CTT | GAT | CAT | TAC | AAA | TAT | CTT | ACT | GCA | TGG | TTG | AAC | TTC | TTA | ATT | 336 |
| Leu | Leu | Asp | His | Tyr | Lys | Tyr | Leu | Thr | Ala | Trp | Leu | Asn | Phe | Leu | Ile | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| TAC | CAA | AGA | AGA | TCA | TTT | TTT | GTC | GGC | CAT | GAT | TGG | GGT | GCT | TGT | TTG | 384 |
| Tyr | Gln | Arg | Arg | Ser | Phe | Phe | Val | Gly | His | Asp | Trp | Gly | Ala | Cys | Leu | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| GCA | TTT | CAT | TAT | AGC | TAT | GAG | CAT | CAA | GAT | AAG | ATC | AAA | GCA | ATA | GTT | 432 |
| Ala | Phe | His | Tyr | Ser | Tyr | Glu | His | Gln | Asp | Lys | Ile | Lys | Ala | Ile | Val | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| CAC | GCT | GAA | AGT | GTA | GTA | GAT | GTG | ATT | GAA | TCA | TGG | GAT | GAA | TGG | CCT | 480 |
| His | Ala | Glu | Ser | Val | Val | Asp | Val | Ile | Glu | Ser | Trp | Asp | Glu | Trp | Pro | |
| 145 | | | | 150 | | | | | | 155 | | | | 160 | | |
| GAT | ATT | GAA | GAA | GAT | ATT | GCG | TTG | ATC | AAA | TCT | GAA | GAA | GGA | GAA | AAA | 528 |
| Asp | Ile | Glu | Glu | Asp | Ile | Ala | Leu | Ile | Lys | Ser | Glu | Glu | Gly | Glu | Lys | |
| | | | | 165 | | | | | 170 | | | | 175 | | | |
| ATG | GTT | TTG | GAG | AAT | AAC | TTC | TTC | GTG | GAA | ACC | ATG | TTG | CCA | TCA | AAA | 576 |
| Met | Val | Leu | Glu | Asn | Asn | Phe | Phe | Val | Glu | Thr | Met | Leu | Pro | Ser | Lys | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| ATC | ATG | AGA | AAG | TTA | GAA | CCA | GAA | GAA | TTT | GCA | GCA | TAT | CTT | GAA | CCA | 624 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Met | Arg | Lys | Leu | Glu | Pro | Glu | Glu | Phe | Ala | Ala | Tyr | Leu | Glu | Pro | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| TTC | AAA | GAG | AAA | GGT | GAA | GTT | CGT | CGT | CCA | ACA | TTA | TCA | TGG | CCT | CGT | 672 | |
| Phe | Lys | Glu | Lys | Gly | Glu | Val | Arg | Arg | Pro | Thr | Leu | Ser | Trp | Pro | Arg | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| GAA | ATC | CCG | TTA | GTA | AAA | GGT | GGT | AAA | CCT | GAC | GTT | GTA | CAA | ATT | GTT | 720 | |
| Glu | Ile | Pro | Leu | Val | Lys | Gly | Gly | Lys | Pro | Asp | Val | Val | Gln | Ile | Val | | |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 | | |
| AGG | AAT | TAT | AAT | GCT | TAT | CTA | CGT | GCA | AGT | GAT | GAT | TTA | CCA | AAA | ATG | 768 | |
| Arg | Asn | Tyr | Asn | Ala | Tyr | Leu | Arg | Ala | Ser | Asp | Asp | Leu | Pro | Lys | Met | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| TTT | ATT | GAA | TCG | GAT | CCA | GGA | TTC | TTT | TCC | AAT | GCT | ATT | GTT | GAA | GGC | 816 | |
| Phe | Ile | Glu | Ser | Asp | Pro | Gly | Phe | Phe | Ser | Asn | Ala | Ile | Val | Glu | Gly | | |
| | | | 260 | | | | 265 | | | | | | 270 | | | | |
| GCC | AAG | AAG | TTT | CCT | AAT | ACT | GAA | TTT | GTC | AAA | GTA | AAA | GGT | CTT | CAT | 864 | |
| Ala | Lys | Lys | Phe | Pro | Asn | Thr | Glu | Phe | Val | Lys | Val | Lys | Gly | Leu | His | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | |
| TTT | TCG | CAA | GAA | GAT | GCA | CCT | GAT | GAA | ATG | GGA | AAA | TAT | ATC | AAA | TCG | 912 | |
| Phe | Ser | Gln | Glu | Asp | Ala | Pro | Asp | Glu | Met | Gly | Lys | Tyr | Ile | Lys | Ser | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | |
| TTC | GTT | GAG | CGA | GTT | CTC | AAA | AAT | GAA | CAA | TAA | | | | | | 945 | |
| Phe | Val | Glu | Arg | Val | Leu | Lys | Asn | Glu | Gln | | | | | | | | |
| | 305 | | | | 310 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCCTG

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTAC

30

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | | | | | | |
|-------------|-------------|------------|------------|------------|------------|------|
| CCTCCACGCA | CGTTGTGATA | TGTAGATGAT | AATCATTATC | AGAGCAGCGT | TGGGGGATAA | 60 |
| TGTCGACATT | TCCACTCCCA | ATGACGGTGA | TGTATAATGC | TCAAGTATTC | TCCTGCTTTT | 120 |
| TTACCACTAA | CTAGGAAGTG | GGTTTGGCCT | TAATTCAGAC | AGCCTTGGCT | CTGTCTGGAC | 180 |
| AGGTCCAGAT | GACTGACACC | ATTAACACTT | TGTCAGCCTC | AGTGACTACA | GTCATAGATG | 240 |
| AACAGGCCCTC | AGCTAATGTC | AAGATACAGA | GAGGTCTCAT | GCTGGTTAAT | CAACTCATAG | 300 |
| ATCTTGTCCA | GATACAACATA | GATGTATTAT | GACAAATAAC | TCAGCAGGGA | TGTGAACAAA | 360 |
| AGTTTCCGGG | ATTGTGTGTT | ATTTCCATTC | AGTATGTTAA | ATTTACTAGG | ACAGCTAATT | 420 |
| TGTCAAAAAG | TCTTTTTCAG | TATATGTTAC | AGAATTGGAT | GGCTGAATTT | GAACAGATCC | 480 |
| TTCGGGAATT | GAGACTTCAG | GTCAACTCCA | CGCGCTTGGA | CCTGTCGCTG | ACCAAAGGAT | 540 |
| TACCCAATTG | GATCTCCTCA | GCATTTTCTT | TCTTTAAAAA | ATGGGTGGGA | TTAATATTAT | 600 |
| TTGGAGATAC | ACTTTGCTGT | GGATTAGTGT | TGCTTCTTTG | ATTGGTCTGT | AAGCTTAAGG | 660 |
| CCCAAAC TAG | GAGAGACAAG | GTGGTTATTG | CCCAGGCGCT | TGCAGGACTA | GAACATGGAG | 720 |
| CTTCCCCTGA | TATATGGTTA | TCTATGCTTA | GGCAATAGGT | CGCTGGCCAC | TCAGCTCTTA | 780 |
| TATCCCACGA | GGCTAGTCTC | ATTGTACGGG | ATAGAGTGAG | TGTGCTTCAG | CAGCCCGAGA | 840 |
| GAGTTGCAAG | GCTAAGCACT | GCAATGGAAA | GGCTCTGCGG | CATATATGTG | CCTATTCTAG | 900 |
| GGGGACATGT | CATCTTTCAT | GAAGGTTTCT | TGTCCTAGTT | CCCTTCCCCC | AGGCAAAACG | 960 |
| ACACGGGAGC | AGGTCAGGGT | TGCTCTGGGT | AAAAGCCTGT | GAGCCTGGGA | GCTAATCCTG | 1020 |
| TACATGGCTC | CTTTACCTAC | ACACTGGGGA | TTTGACCTCT | ATCTCCACTC | TCATTAATAT | 1080 |
| GGGTGGCCTA | TTTGCTCTTA | TTAAAAGGAA | AGGGGGAGAT | GTTGGGAGCC | GCGCCACAT | 1140 |
| TCGCCGTTAC | AAGATGGCGC | TGACAGCTGT | GTTCTAAGTG | GTAAACAAAT | AATCTGCGCA | 1200 |
| TGTGCCGAGG | GTGGTTCTTC | ACTCCATGTG | CTCTGCCTTC | CCCGTGACGT | CAACTCGGCC | 1260 |
| GATGGGCTGC | AGCCAATCAG | GGAGTGACAC | GTCTTAGGCG | AAGGAGAATT | CTCCTTAATA | 1320 |
| GGGACGGGGT | TTCGTTCTCT | CTCTCTCTCT | TGCTTCTCTC | TCTTGCTTTT | TCGCTCTCTT | 1380 |
| GCTTCCCCTA | AAGTGATAAT | GATTATCATC | TACATATCAC | AACGTGCGTG | GAGG | 1434 |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| CCTCCACGCA | CGTTGTGATA | TGTAGATGAT | AATCATTATC | AGAGCAGCGT | TGGGGGATAA | 60 |
| TGTCGACATT | TCCACTCCCA | ATGACGGTGA | TGTATAATGC | TCAAGTATTC | TCCTGCTTTT | 120 |
| TTACCACTAA | CTAGGAAGTG | GGTTTGGCCT | TAATTCAGAC | AGCCTTGGCT | CTGTCTGGAC | 180 |
| AGGTCCAGAT | ACAAC TAGAT | GTATTATGAC | AAATAACTCA | GCAGGGATGT | GAACAAAAGT | 240 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| TTCCGGGATT | GCGTGTTATT | TCCATCCAGT | ATGTTAAATT | TACTAGGGCA | GCTAATTTGT | 300 |
| CAAAAAGTCT | TTTCCAGTAT | ATGTTACAGA | ATTGGATGGC | TGAATTTGAA | CAGATCCTTC | 360 |
| GGGAATTGAG | ACTTCAGGTC | AACTCCACGC | GCTTGACCT | GTCCCTGACC | AAAGGATTAC | 420 |
| CCAATTGGAT | CTCCTCAGCA | TTTTCTTTCT | TTAAAAAATG | GGTGGGATTA | ATATTATTTG | 480 |
| GAGATACACT | TTGCTGTGGA | TTAGTGTTCG | TTCTTTGATT | GGTCTGTAAG | CCTAAGGCCC | 540 |
| AAACTAGGAG | AGACAAGGTG | GTTATTGCCC | AGGCGCTTGC | AGGACTAGAA | CATGGAGCTT | 600 |
| CCCCTGATAT | ATCTATGCTT | AGGCAATAGG | TCGCTGGCCA | CTCAGCTCTT | ATATCCCATG | 660 |
| AGGCTAGTCT | CATTGCACGG | GATAGAGTGA | GTGTGCTTCA | GCAGCCCGAG | AGAGTTGCAC | 720 |
| GGCTAAGCAC | TGCAATGGAA | AGGCTCTGCG | GCATATATGA | GCCTATTCTA | GGGAGACATG | 780 |
| TCATCTTTCA | AGAAGGTTGA | GTGTCCAAGT | GTCTTCCCTC | CAGGCAAAAC | GACACGGGAG | 840 |
| CAGGTCAGGG | TTGCTCTGGG | TAAAAGCCTG | TGAGCCTAAG | AGCTAATCCT | GTACATGGCT | 900 |
| CCTTTACCTA | CACACTGGGG | ATTTGACCTC | TATCTCCACT | CTCATTAATA | TGGGTGGCCT | 960 |
| ATTTGCTCTT | ATTAAAAGGA | AAGGGGGAGA | TGTTGGGAGC | CGCGCCCA | TTCGCCGTTA | 1020 |
| CAAGATGGCG | CTGACAGCTG | TGTTCTAAGT | GGTAAACAAA | TAATCTGCGC | ATGCGCCGAG | 1080 |
| GGTGGTTCTT | CACCTCATGT | GCTCTGCCTT | CCCCGTGACG | TCAACTCGGC | CGATGGGCTG | 1140 |
| CAGTCAATCA | GGGAGTGACA | CGTCCTAGGC | GAAGGAAAAT | TCTCCTTAAT | AGGGACGGGG | 1200 |
| TTTCGTTTTC | TCTCTCTCTT | GCTTCGCTCT | CTCTTGCTTC | TTGCTCTCTT | TTCCTGAAGA | 1260 |
| TGTAAGAATA | AAGCTTTGCC | GCAGAAGATT | CTGGTCTGTG | GTGTTCTTCC | TGGCCGGTCG | 1320 |
| TGAGAACGCG | TCTAATAACA | ATTGGTGCCG | AAACCCGGGT | GATAATGATT | ATCATCTACA | 1380 |
| TATCACAACG | TGCGTGGAGG | | | | | 1400 |

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

| | | | | | | |
|-------------|------------|------------|-------------|------------|------------|------|
| CCTCCACGCA | CGTTGTGATA | TGTAGATGAT | AATCATTATC | ACTTTACGGG | TCCTTTCACT | 60 |
| ACAACTGCCA | CGAGGCCCGG | TGCTCTGGTA | ATAGATCTTT | GCTGAAAAGG | CACACACATG | 120 |
| ACACATTACT | CAAGGTGGGC | TCATCTGAGC | TGCAGATTCA | GCTTAATATG | AATCTTGCCA | 180 |
| ATTGTGTGAA | ATCATAAATC | TTCAAAGTGA | CACTCATTGC | CAGACACAGG | TGCCCACCTT | 240 |
| TGGCATAATA | AACAAACACA | AATTATCTAT | TATATAAAGG | GTGTTAGAAG | ATGCTTTAGA | 300 |
| ATACAAATAA | ATCATGGTAG | ATAACAGTAA | GTTGAGAGCT | TAAATTTAAT | AAAGTGATAT | 360 |
| ACCTAATAAA | AATTAATAA | AGAAGGTGTG | AATATACTAC | AGTAGGTAAA | TTATTTCACT | 420 |
| AATTTATTTT | CTTTCTTAAT | CCTTTATAAT | GTTTTCTGCT | ATTGTCAATT | GCACATCCAT | 480 |
| ATGTTCAATT | CTTCACTGTA | ATGAAGAAAT | GTAGTAAATA | TACTTTCCGA | ACAAGTTGTA | 540 |
| TCAAATATGT | TACACTTGAT | TCCGTGTGTT | ACTTATCACT | TTATTATTAT | ATTGATTGCA | 600 |
| TTCTTTCGTT | ACTTGATATT | ATTACAAGGT | ACATATTTAT | TCTCTCAGAT | CTTCATTATA | 660 |
| CTCTAACCAT | TTTATAACAT | ACTTTATTTA | TTCATTTCTT | ATGTGTGCTG | TGAGGCACAA | 720 |
| ATGCCAGAGA | GAACCTGAGC | AGATAAGAGG | ACAAATTGCA | AGAGTCAGTT | ACCTCCTGCT | 780 |
| GTTCCCTTGA | AACTCAGGAT | CAAATTCAGG | TTGTCAGGCT | TGGCAGCATG | CACTTTTTAC | 840 |
| CAGTGCCCTC | ATCTTGCTAG | CCCTGAACAT | CAAGCTTTGC | AGACAGACAG | GCTACACTAA | 900 |
| GTGAACCTGGT | CATTCACAGC | ATGCATGGTG | ATTTATTGTT | ACTTTCTATT | CCATGCCTTT | 960 |
| ACTATTTCTA | CTAGGTGCTA | GCTAGTACTG | TATTTTCGAGA | TAGAAGTTAC | TGAAAGAAAA | 1020 |
| TTACATTGTT | TTCTATAGAT | CCTTGATACT | CTTTCAGCAG | ATATAGAGTT | TTAATCAGGT | 1080 |
| CCTAGACCTT | TTCTTCACTC | TTATTAAATA | CTAAGTACAA | ATTAAGTTTA | TCCAAAACAG | 1140 |
| TACGGATGTT | GATTTTGTGC | AGTTCTACTA | TGATAATAGT | CTAGCTTCAT | AAATCTGACA | 1200 |
| CACTTATTGG | GAATGTTTTT | GTTAATAAAA | GATTCAGGTG | TTACTCTAGG | TCAAGAGAAT | 1260 |
| ATTAAACATC | AGTCCCAAAT | TACAACTTTC | AATAAAAGAT | TTGACTCTCC | AGTGGTGGCA | 1320 |
| ATATAAAGTG | ATAATGATTA | TCATCTACAT | ATCACAACGT | GCGTGGAGG | | 1369 |

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22118 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

| | | | | | | |
|-------------|------------|-------------|------------|------------|------------|------|
| GAATTCCCCT | ATCCCTAATC | CAGATTGGTG | GAATAACTTG | GTATAGATGT | TTGTGCATTA | 60 |
| AAAACCCGTG | AGGATCTTCA | CTCTAGGTCA | CTGTTCAGCA | CTGGAACCTG | AATTGTGGCC | 120 |
| CTGAGTGATA | GGTCCTGGGA | CATATGCAGT | TCTGCACAGA | CAGACAGACA | GACAGACAGA | 180 |
| CAGACAGACA | GACAGACGTT | ACAAACAAAC | ACGTTGAGCC | GTGTGCCAAC | ACACACACAA | 240 |
| ACACCACTCT | GGCCATAATT | ATTGAGGACG | TTGATTTATT | ATTCTGTGTT | TGTGAGTCTG | 300 |
| TCTGTCTGTC | TGTCTGTCTG | TCTGTCTGTC | TATCAAACCA | AAAGAAACCA | AACAATTATG | 360 |
| CCTGCCTGCC | TGCCTGCCTG | CCTACACAGA | GAAATGATTT | CTTCAATCAA | TCTAAAACGA | 420 |
| CCTCCTAAGT | TTGCCTTTTT | TCTCTTTCTT | TATCTTTTTT | TTTTTTCTTT | TCTTCTTCTT | 480 |
| TCCTTCTTCT | CTTCTTCTCT | TCCTTCTTCT | CTTCTTCTCT | TTCTTTCTTT | CTTACTTTCT | 540 |
| TTCTTTCTCT | CTTACATTTA | TTCTTTTTCAT | ACATAGTTTC | TTAGTGTAAG | CATCCCTGAC | 600 |
| TGTCTTGAAG | ACACTTTTGT | GGCCTCAATC | CTGTAAGAGC | CTTCCTCTGC | TTTTCAAATG | 660 |
| CTGGCATGAA | TGTTGTACCT | CACATATGACC | AGCTTAGTCT | TCAAGTCTGA | GTTACTGGAA | 720 |
| AGGAGTTCCA | AGAAGACTGG | TTATATTTTT | CATTTATTAT | TGCATTTTAA | TTAAAATTTA | 780 |
| ATTTACCAA | AAGAATTTAG | ACTGACCAAT | TCAGAGTCTG | CCGTTTAAAA | GCATAAGGAA | 840 |
| AAAGTAGGAG | AAAAACGTGA | GGCTGTCTGT | GGATGGTCGA | GGCTGCTTTA | GGGAGCCTCG | 900 |
| TCACCATTCT | GCACTTGCAA | ACCGGGCCAC | TAGAACCCGG | TGAAGGGAGA | AACCAAAGCG | 960 |
| ACCTGGA AAC | AATAGGTCAC | ATGAAGGCCA | GCCACCTCCA | TCTTGTTGTG | CGGGAGTTCA | 1020 |
| GTTAGCAGAC | AAGATGGCTG | CCATGCACAT | GTTGTCTTTC | AGCTTGGTGA | GGTCAAAGTA | 1080 |
| CAACCGAGTC | ACAGAACAAG | GAAGTATACA | CAGTGAGTTC | CAGGTCAGCC | AGAGTTTACA | 1140 |
| CAGAGAAACC | ACATCTTGAA | AAAAACAAAA | AAATAAATTA | AATAAATATA | ATTTAAAAAT | 1200 |
| TTAAAAATAG | CCGGGAGTGA | TGGCGCATGT | CTTTAATCCC | AGCTCTCTTC | AGGCAGAGAT | 1260 |
| GGGAGGATTT | CTGAGTTTGA | GGCCAGCCTG | GTCTGCAAAG | TGAGTTCAG | GACAGTCAGG | 1320 |
| GCTATACAGA | GAAACCCGTG | CTTGAAAAC | AAACTAAATT | AAACTAAACT | AAACTAAAAA | 1380 |
| AATATAAAAT | AAAAATTTTA | AAGAATTTTA | AAAAACTACA | GAAATCAAAC | ATAAGCCCAC | 1440 |
| GAGATGGCAA | GTAACCTGCA | TCATAGCAGA | AATATTATAC | ACACACACAC | ACACAGACTC | 1500 |
| TGTCATAAAA | TCCAATGTGC | CTTCATGATG | ATCAAATTTT | GATAGTCAGT | AATACTAGAA | 1560 |
| GAATCATATG | TCTGAAAATA | AAAGCCAGAA | CCTTTTCTGC | TTTTGTTTTT | TTTTGCCCCA | 1620 |
| AGATAGGGTT | TCTCTCAGTG | TATCCCTGGC | ATCCCTGCCT | GGAACCTTCT | TTGTAGGTTT | 1680 |
| GGTAGCCTCA | AACTCAGAGA | GGTCCTCTCT | GCCTGCCTGC | CTGCCTGCCT | GCCTGCCTGC | 1740 |
| CTGCCTGCCT | GCCTGCCTCA | CTTCTTCTGC | CACCCACACA | ACCGAGTCGA | ACCTAGGATC | 1800 |
| TTTATTTCTT | TCTCTTTCTC | TCTTCTTTCT | TTCTTTCTTT | CTTTCTTTCT | TTCTTTCTTT | 1860 |
| CTTCTTTCTT | TTCTTTATTC | ATTAGTTTTT | AATGTAAGTG | TGTGTTTGTG | CTCTATCTGC | 1920 |
| TGCCTATAGG | CCTGCTTGCC | AGGAGAGGGC | AACAGAACCT | AGGAGAAACC | ACCATGCAGC | 1980 |
| TCCTGAGAAT | AAGTGAAAAA | ACAACAAAAA | AAGGAAATTC | TAATCACATA | GAATGTAGAT | 2040 |
| ATATGCCGAG | GCTGTCAGAG | TGCTTTTTTA | GGCTTAGTGT | AAGTAATGAA | AATTGTTGTG | 2100 |
| TGTCTTTTAT | CCAAACACAG | AAGAGAGGTG | GCTCGGCTG | CATGTCTGTT | GTCTGCATGT | 2160 |
| AGACCAGGCT | GGCCTTGAAC | ACATTAATCT | GTCTGCCTCT | GCTTCCCTAA | TGCTGCGATT | 2220 |
| AAAGGCATGT | GCCACCACCT | CCCGGACTGA | TTTCTTCTTT | TTTTTTTTTT | TGGAAAATAC | 2280 |
| CTTTCTTTCT | TTTCTCTCTT | CTCTTTCTTC | CTTCTTCTCT | TTCTTTCTAT | TCTTTTTTTC | 2340 |
| TTTCTTTTTT | CTTTTTTTTT | TTTTTTTTTA | AAATTGCCTA | AGGTTAAAGG | TGTGCTCCAC | 2400 |
| AATTGCCTCA | GCTCTGCTCT | AATTCTCTTT | AAAAAAAAAA | AAACAAAAAA | AAAACCAAAA | 2460 |
| CAGTATGTAT | GTATGTATAT | TTAGAAGAAA | TACTAATCCA | TTAATAACTC | TTTTTTTCTA | 2520 |
| AAATTCATGT | CATTCTTGTT | CCACAAAGTG | AGTTCCAGGA | CTTACCAGAG | AAACCCTGTG | 2580 |
| TTCAAATTTT | TGTGTTCAAG | GTCACCCCTG | CTTACAAAGT | GAGTTCCAAG | TCCGATAGGG | 2640 |
| CTACACAGAA | AAACCATATC | TCAGAAAAAA | AAAAAGTTCC | AAACACACAC | ACACACACAC | 2700 |
| ACACACACAC | ACACACACAC | ACACACACAC | ACACACACAG | CGCGCCGCGG | CGATGAGGGG | 2760 |
| AAGTCGTGCC | TAAAATAAAT | ATTTTTCTGG | CCAAAGTGAA | AGCAAATCAC | TATGAAGAGG | 2820 |
| TACTCCTAGA | AAAAATAAAT | ACAAACGGGC | TTTTTAATCA | TTCCAGCACT | GTTTTAATTT | 2880 |
| AACTCTGAAT | TTAGTCTTGG | AAAAGGGGGG | GGGTGTGGGT | GAGTGAGGGC | GAGCGAGCAG | 2940 |
| ACGGGCGGGC | GGGCGGGTGA | TGGGCGGGC | GCGGTGGCAG | CGAGCACCAG | AAAACAACAA | 3000 |
| ACCCCAAGCG | GTAGAGTGTT | TTAAAAATGA | GACCTAAATG | TGGTGGAACG | GAGGTGCGCC | 3060 |
| CCACCCTCCT | CTTCCACTGC | TTAGATGCTC | CCTTCCCCTT | ACTGTGCTCC | CTTCCCCTAA | 3120 |
| CTGTGCCTAA | CTGTGCCTGT | TCCCTCACCC | CGCTGATTGC | CCAGCGACGT | ACTTTGACTT | 3180 |

| | | | | | | |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| CAAGAACGAT | TTTGCCTGTT | TTCACCGCTC | CCTGTGCATAC | TTTCGTTTTT | GGGTGCCCGA | 3240 |
| GTCTAGCCCC | TTTCGCTATGT | TCGGGCGGGA | CGATGGGGAC | CGTTTGTGCC | ACTCGGGAGA | 3300 |
| AGTGGTGGGT | GGGTACGCTG | CTCCGTCGTG | CGTGCCTGAG | TGCCGGAACC | TGAGCTCGGG | 3360 |
| AGACCTCCG | GAGAGACAGA | ATGAGTGAGT | GAATGTGGCG | GCGCGTGACG | GATCTGTATT | 3420 |
| GGTTTGTATG | GTTGATCGAG | ACCATTTGTCG | GGCGACACCT | AGTGGTGACA | AGTTTCGGGA | 3480 |
| ACGCTCCAGG | CCTCTCAGGT | TGGTGACACA | GGAGAGGGAA | GTGCCTGTGG | TGAGGCGACC | 3540 |
| AGGGTGACAG | GAGGCCGGGC | AAGCAGGCGG | GAGCGTCTCG | GAGATGGTGT | CGTGTTTAAG | 3600 |
| GACGGTCTCT | AACAAGGAGG | TCGTACAGGG | AGATGGCCAA | AGCAGACCGA | GTTGCTGTAC | 3660 |
| GCCCTTTTGG | GAAAAATGCT | AGGGTTGGTG | GCAACGTTAC | TAGGTGCGACC | AGAAGGCTTA | 3720 |
| AGTCTTACCC | CCCCCCCCCT | TTTTTTTTTT | TTTCTCTCCAG | AAGCCCTCTC | TTGTCCCCGT | 3780 |
| CACCGGGGGG | ACCGTACATC | TGAGGCCGAG | AGGACGCGAT | GGGCCCCGGT | TCCAAGCCGG | 3840 |
| TGTGGCTCGG | CCAGCTGGCG | CTTCGGGTCT | TTTTTTTTTT | TTTTTTTTTT | TTTTCTCTCA | 3900 |
| GAAGCCTTGT | CTGTCGCTGT | CACCGGGGGC | GCTGTACTTC | TGAGGCCGAG | AGGACGCGAT | 3960 |
| GGGCCCCGGC | TTCCAAGCCG | GTGTGGCTCG | GCCAGCTGGA | GCTTCGGGTC | TTTTTTTTTT | 4020 |
| TTTTTTTTTT | TTTTTTTCTC | CAGAAGCCTT | GTCTGTGCTG | GTCACCGGGG | GCGCTGTACT | 4080 |
| TCTGAGGCCG | AGAGGACGCG | ATGGGTCTGGC | TTCCAAGCCG | ATGTGGCGGG | GCCAGCTGGA | 4140 |
| GCTTCGGGTT | TTTTTTTTTT | CTCCAGAAGC | CCTCTCTTGT | CCCCGTCACC | GGGGGCGCTG | 4200 |
| TACTTCTGAG | GCCGAGAGGA | CGTGATGGGC | CCGGGTTCCA | GGCGGATGTC | GCCCGGTCAG | 4260 |
| CTGGAGCTTT | GGATCTTTTT | TTTTTTTTTT | CCTCCAGAAG | CCCTCTCTTG | TCCCCGTCAC | 4320 |
| CGGGGGCACC | TTACATCTGA | GGGCGAGAGG | ACGTGATGGG | TCCGGCTTCC | AAGCCGATGT | 4380 |
| GGCGGGGCCA | GCTGGAGCTT | CGGGTTTTTT | TTTTTTTCTC | CAGAAGCCCT | CTCTTGTCCC | 4440 |
| CGTCACCGGG | GGCGCTGTAC | TTCTGAGGCC | GAGAGGACGT | GATGGGCCCC | GGTTCAGGC | 4500 |
| GGATGTCGCC | CGGTACAGCTG | GAGCTTTGGA | TCATTTTTTT | TTTTCCCTCC | AGAAGCCCTC | 4560 |
| TCTTGTCCCC | GTCACCGGGG | GCACCGTACA | TCTGAGGCCG | AGAGGACACG | ATGGGCTCTG | 4620 |
| CTTCCAAGCC | GATGTGGCCC | GGCCAGCTGG | AGCTTCGGGT | CTTTTTTTTT | TTTTTCTCTC | 4680 |
| CAGAAGCCTT | GTCTGTGCTG | GTCACCGGGG | GCGCTGTACT | TCTGAGGCCG | AGAGGACGCG | 4740 |
| ATGGGCCCCG | CTTCCAAGCC | GGTGTGGCTC | GGCCAGCTGG | AGCTTCGGGT | CTTTTTTTTT | 4800 |
| TTTTTTTTTT | TTCTCTCCAG | AACCTTGTCT | GTGCTGTGCA | CCCCGGGCGC | TTGTACTTCT | 4860 |
| GATGCCGAGA | GGACGCGATG | GGCCCGTCTT | CCAGGCCGAT | GTGGCCCCGG | CAGCTGGAGC | 4920 |
| TTTGGATCTT | TTTTTTTTTT | TTTTCTCTCA | GAAGCCCTCT | CTTGTCCCCG | TCACCGGGGG | 4980 |
| CACCTTACAT | CTGAGGCCTA | GAGGACACGA | TGGGCCCGGG | TTCCAGGCCG | ATGTGGCCCC | 5040 |
| GTCAGCTGGA | GCTTTGGATC | TTTTTTTTTT | TTTTCTTCCA | GAAGCCCTCT | TGTCCCCGTC | 5100 |
| ACCGGTGGCA | CTGTACATCT | GAGGCGGAGA | GGACATTATG | GGCCCCGGCT | CCAATCCGAT | 5160 |
| GTGGCCCCGT | CAGCTGGAGC | TTTGGATCTT | ATTTTTTTTT | TAATTTTTTT | TTCCAGAGC | 5220 |
| CCTCTTGTC | CTGTCACCGG | TGGCACGGTA | CATCTGAGGC | CGAGAGGACA | TTATGGGCC | 5280 |
| GGCTTCCAGG | CCGATGTGGC | CCGGTCAGCT | GGAGCTTTGG | ATCTTTTTTT | TTTTTTTTTCT | 5340 |
| TTTTTCTCTC | AGAAGCCCTC | TCTGTCCCTG | TCACCGGGGG | CCCTGTACGT | CTGAGGCCGA | 5400 |
| GGGAAAGCTA | TGGGCGCGGT | TTTCTTTTAT | TGACCTGTCT | GTCTTATCAG | TTCTCCGGGT | 5460 |
| TGTCAGGGTC | GACCAGTTGT | TCTTTTGGAG | TCCGGTTCTT | TTCTGTTATG | GGTCATTTTT | 5520 |
| GGGCCACCTC | CCCAGGTATG | ACTTCCAGGC | GTCGTTGCTC | GCCTGTCACT | TTCTTCCCTG | 5580 |
| TCTCTTTTAT | GCTTGTGATC | TTTTCTATCT | GTTCTTATTG | GACCTGGAGA | TAGGTACTGA | 5640 |
| CACGCTGTCC | TTTCCCTATT | AACACTAAAG | GACACTATAA | AGAGACCCCT | TCGATTTAAG | 5700 |
| GCTGTTTTGC | TTGTCCAGCC | TATTCTTTTT | ACTGGCTTGG | GTCTGTGCGG | GTGCTGAAG | 5760 |
| CTGTCCCCGA | GCCACGCTTC | CTGCTTTCCC | GGGCTTGCTG | CTTGCCTGTG | CTTGCCTGTG | 5820 |
| GCAGCTTGTG | ACAACCTGGG | GCTGTGACTT | TGCTGCGTGT | CAGACGTTTT | TCCCGATTTT | 5880 |
| CCCGAGGTGT | CGTTGTACAC | CCTGTCCCGG | TTGGAATGGT | GGAGCCAGCT | GTGGTTGAGG | 5940 |
| GCCACCTTAT | TTCCGGCTCAC | TTTTTTTTTT | TTTTTTTCTC | TTGGAGTCCC | GAACCTCCGC | 6000 |
| TCTTTTCTCT | TCCCGGTCTT | TCTTCCACAT | GCCTCCCGAG | TGCATTTCTT | TTTGTTTTTT | 6060 |
| TTCTTTTTTT | TTTTTTTTTT | TTGGGGAGGT | GGAGAGTCCC | GAGTACTTCA | CTCCTGTCTG | 6120 |
| TGGTGTCCAA | GTGTTTCATG | CACGTGCCTC | CCGAGTGCAC | TTTTTTTTTGT | GGCAGTCGCT | 6180 |
| CGTTGTGTTT | TCTTGTCTCT | TGTCTGCCCC | TATCAGTAAC | TGTCTTGCCC | CGCGTGTAA | 6240 |
| ACATTCTTAT | CTCGCTTGTT | TCTCCCGATT | GCGCGTCTGT | GCTCACTCTT | AGATCGATGT | 6300 |
| GGTGTCTCCG | AGTTCTCTTC | GGGCCAGGGC | CAAGCCGCGC | CAGGCGAGGG | ACGGACATTC | 6360 |
| ATGGCGAATG | GCGGCCGCTC | TTCTCGTTCT | GCCAGCGGGC | CCTCGTCTCT | CCACCCCATC | 6420 |
| CGTCTGCCGG | TGGTGTGTGG | AAGGCAGGGG | TGCGGCTCTC | CGGCCCCGAC | CTGCCCCGCG | 6480 |
| CGCACTTTTC | TCAGTGGTTC | GCGTGGTCCT | TGTGGATGTG | TGAGGCGCCC | GGTTGTGCCC | 6540 |
| TCACGTGTTT | CACTTTGGTC | GTGTCTCGCT | TGACCATGTT | CCCAGAGTCG | GTGGATGTGG | 6600 |
| CCGTGGCGGT | TGCATACCTT | TCCCGTCTGG | TGTGTGCACG | CGCTGTTTCT | TGTAAGCGTC | 6660 |
| GAGGTGCTCC | TGGAGCGTTC | CAGGTTTGTG | TCCTAGGTGC | CTGCTTCTGA | GCTGGTGGTG | 6720 |
| GCGCTCCCCA | TTCCCTGGTG | TGCCTCCGGT | GCTCCGCTCT | GCTGTGTGCC | TTCCCGTTTG | 6780 |
| TGCTTGAGAA | GCCCCGTGAG | GGGGGGTCGA | GGAGAGAAGG | AGGGGCAAGA | CCCCCTTCT | 6840 |
| TCGTGCGGTG | AGGCGCCAC | CCCGCGACTA | GTACGCTGT | GCGTAGGGCT | GGTGTCTGAG | 6900 |
| GTCGCGGCT | GGGGTTGGAA | AGTTTCTCGA | GAGACTCATT | GCTTTCCCGT | GGGGAGCTTT | 6960 |
| GAGAGGCCTG | GCTTTCGGGG | GGGACCGGTT | GCAGGGTCTC | CCCTGTCCGC | GGATGCTCAG | 7020 |
| AATGCCCTTG | GAAGAGAACC | TTCCTGTTGC | CGCAGACCCC | CCCCGCGGGT | CGCCCGCGTG | 7080 |

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|-------------|------------|-------------|------------|-------------|-------------|-------|
| TTGGTCTTCT | GTTTCCCTG | TGTGCTCGTC | GCATGCATCC | TCTCTCGGTG | GCCGGGGCTC | 7140 |
| GTCGGGGTTT | TGGGTCCGTC | CCGCCCTCAG | TGAGAAAGTT | TCCTTCTCTA | GCTATCTTCC | 7200 |
| GGAAAGGGTG | CGGGCTTCTT | ACGGTCTCGA | GGGGTCTCTC | CCGAATGGTC | CCCTGGAGGG | 7260 |
| CTCGCCCCCT | GACCGCCTCC | CGCGCGCGCA | GCGTTTGCTC | TCTCGTCTAC | CGCGGCCCGC | 7320 |
| GGCCTCCCCG | CTCCGAGTTC | GGGGAGGGAT | CACGCGGGGC | AGAGCCTGTC | TGTCGTCCCTG | 7380 |
| CCGTGTGCTG | GGAGCATGTG | GCTCGGCTTG | TGTGGTTGGT | GGCTGGGGAG | AGGGCTCCGT | 7440 |
| GCACACCCCC | GCGTGC CGT | ACTTTCCTCC | CCTCCTGAGG | GCCGCCGTGC | GGACGGGGTG | 7500 |
| TGGGTAGGCG | ACGGTGGGCT | CCCGGGTCCC | CACCCGTCTT | CCCGTGCCTC | ACCCGTGCCT | 7560 |
| TCCGTCGCGT | GCGTCCCTCT | CGCTCGCGTC | CACGACTTTG | GCCGCTCCCG | CGACGGCGGC | 7620 |
| CTGCGCCGCG | CGTGGTGCGT | GCTGTGTGCT | TCTCGGGCTG | TGTGGTTGTG | TCGCCTCGCC | 7680 |
| CCCCCTTCC | CGCGGCAGCG | TTCCACGGC | TGGCGAAATC | GCGGGAGTCC | TCCTTCCCTT | 7740 |
| CCTCCGGGTC | GAGAGGGTCC | GTGTCTGGCG | TTGATTGATC | TCGCTCTCGG | GGACGGGACC | 7800 |
| GTTCTGTGGG | AGAACGGCTG | TTGGCCGCGT | CCGGCGCGAC | GTCGGACGTG | GGGACCCACT | 7860 |
| GCCGCTCGGG | GGTCTTTCGT | GGTAGGCATC | GGTGTGTGCG | CATCGGTCTC | TCTCTCGTGT | 7920 |
| CGGTGTCGCC | TCCTCGGGCT | CCCGGGGGGC | CGTCGTGTTT | CGGGTCGGCT | CGGCGCTGCA | 7980 |
| GGTGTGGTGG | GACTGCTCAG | GGGAGTGGTG | CAGTGTGATT | CCCGCCGGTT | TTGCCTCGCG | 8040 |
| TGCCCTGACC | GGTCCGACGC | CCGAGCGGTC | TCTCGGTCCC | TTGTGAGGAC | CCCCTTCCGG | 8100 |
| GAGGGGCCCC | TTTCGGCCGC | CCTTGCCGTC | GTCGCCGGCC | CTCGTTCTGC | TGTGTGCTTC | 8160 |
| CCCCCTCCCC | GCTCGCCGCA | GCCGGTCTTT | TTTCTCTCT | CCCCCCTCT | CCTCTGACTG | 8220 |
| ACCCGTGGCC | GTGCTGTGCG | ACCCCCCGCA | TGGGGGCGGC | CGGGCACGTA | CGCGTCCGGG | 8280 |
| CGGTACCGCG | GTCCTTGGGG | GGGGGCGGAG | GGTAAGAAA | GTCGGCTCGG | CGGGCGGGAG | 8340 |
| GAGCTGTGGT | TTGGAGGGCG | TCCCGGCCCC | GCGGCCGTGG | CGGTGTCTTG | CGCGGTCTTG | 8400 |
| GAGAGGGCTG | CGTGCGAGGG | GAAAAGGTTG | CCCCGCGAGG | GCAAAGGGAA | AGAGGCTAGC | 8460 |
| AGTGGTCATT | GTCCCACGCG | TGTGGTGGTC | TGTTGGCCGA | GGTGCGTCTG | GGGGGCTCGT | 8520 |
| CCGGCCCTGT | CGTCCGTCGG | GAAGGCGCGT | GTTGGGGCCT | GCCGGAGTGC | CGAGGTGGGT | 8580 |
| ACCTTGGCGG | TGGGATTAAC | CCCGCGCGCG | TGTCCCGGTG | TGGCGGTGGG | GGCTCCGGTC | 8640 |
| GATGTCTACC | TCCCTCTCCC | CGAGGTCTCA | GGCCTTCTCC | GCGCGGGCTC | TCGGCCCTCC | 8700 |
| CCTCGTTTCT | CCCTCTCGCG | GGGTTCAGT | CGCTCGTCCA | CCTCCCTCC | TCCGTCTTTC | 8760 |
| CATCTCTCGC | GCAATGGCGC | CGCCGAGTT | CACGGTGGGT | TCGTCTCTCC | CCTCCGCTTC | 8820 |
| TCGCCGGGGG | CTGGCCGCTG | TCCGGTCTCT | CCTGCCCGAC | CCCCGTTGGC | GTGGTCTTCT | 8880 |
| CTCGCCGGCT | TCGCGGACTC | CTGGCTTCGC | CCGGAGGGTC | AGGGGGCTTC | CCGGTTCCCC | 8940 |
| GACGTTGCGC | CTCGCTGCTG | TGTGCTTGGG | GGGGGCCCCG | TGCGGCCCTC | GCCCCGCCGT | 9000 |
| GAGCCCCCTG | CGCACCCGCC | GGTGTGCGGT | TTTCGCGCCG | GGTCAGTTGG | GCCCTGGCGT | 9060 |
| TGTGTCGCGT | CGGGAGCGTG | TCCGCCTCGC | GGCGGCTAGA | CGCGGGTGTC | GCCGGGTCTC | 9120 |
| GACGGGTGGC | CTATCCAGGG | CTCGCCCCCG | CCGACCCCCG | CCTGCCCGTC | CGCGGTGGTG | 9180 |
| TCGTTGGTGT | GGGGAGTGAA | TGGTGCTACC | GGTCATTCCC | TCCCGCGTGG | TTTGACTGTC | 9240 |
| TCGCCGGTGT | CGCGCTTCTC | TTTCCGCCAA | CCCCCACGCC | AACCCACCAC | CCTGTCTCTC | 9300 |
| CGGCCCGGTG | CGGTTCGACG | TCCGGCTCTC | CCGATGCCGA | GGGGTTCGGG | ATTTGTGCCG | 9360 |
| GGGACGGAGG | GGAGAGCGGG | TAAGAGAGGT | TCGGAGAGC | TGTCCCGGGG | CGACGCTCCG | 9420 |
| GTTGGCTTTG | CCGCGTGCGT | GTGCTCGCGG | ACGGGTTTGT | TCGGACCCCG | ACGGGGTTCG | 9480 |
| TCCGGCCGCA | TGCACTCTCC | CGTTCGCGCG | GAGCGCCCGC | CCGGCTCACC | CCCGGTTTGT | 9540 |
| CCTCCCGCGA | GGCTCTCCGC | CGCCGCCGCC | TCCTCCTCCT | CTCTCGCGCT | CTCTGTCCCG | 9600 |
| CCTGGTCTCT | TCCCACCCCC | GACGCTCCGC | TCGCGCTTCC | TTACCTGGTT | GATCCTGCCA | 9660 |
| GGTAGCATAT | GCTTGTCTCA | AAGATTAAGC | CATGCATGTC | TAAGTACGCA | CGGCCGTATC | 9720 |
| AGTGAAACTG | CGAATGGCTC | ATTAAATCAG | TTATGGTTCC | TTTGGTCGCT | CGTCTCTCTC | 9780 |
| CTACTTGGAT | AACTGTGGTA | ATTCTAGAGC | TAATACATGC | CGACGGGCGC | TGACCCCCCT | 9840 |
| TCCCGGGGGG | GGATGCGTGC | ATTATCAGA | TCAAACCAA | CCCGGTGAGC | TCCCTCCCCG | 9900 |
| CTCCGGCCCG | GGGTCCGGCG | CCGGCGGCTT | GGTGACTCTA | GATAACCTCG | GGCCGATCGC | 9960 |
| ACGCCCCCGG | TGGCGGCGAC | GACCCATTCC | AACGTCTGCC | CTATCAACTT | TCGATGGTAG | 10020 |
| TCGCCGTGCC | TACCATGGTG | ACCACGGGTG | ACGGGGAATC | AGGGTTCGAT | TCCGGAGAGG | 10080 |
| GAGCCTGAGA | AACGGCTACC | ACATCCAAGG | AAGGCAGCAG | GCGCGCAAAT | TACCCACTCC | 10140 |
| CGACCCGGGG | AGGTAGTGAC | GAAAAATAAC | AATACAGGAC | TCTTTCGAGG | CCCTGTAAAT | 10200 |
| GGAATGAGTC | CACTTTAAAT | CCTTTAACGA | GGATCCATTG | GAGGGCAAGT | CTGGTGCCAG | 10260 |
| CAGCCGCGGT | AATTCCAGCT | CCAATAGCGT | ATATTAAAGT | TGCTGCAGTT | AAAAAGCTCG | 10320 |
| TAGTTGGATC | TTGGGAGCGG | GCGGGCGGTC | CGCCGCGAGG | CGAGTCACCG | CCCGTCCCCG | 10380 |
| CCCCTTGCCCT | CTCGGCGCCC | CCTCGATGCT | CTTAGCTGAG | TGTCCCGCGG | GGCCCGAAGC | 10440 |
| GTTTACTTTG | AAAAAATTAG | AGTGTTCAAA | GCAGGCCCCA | GCCGCCTGGA | TACCCAGACT | 10500 |
| AGGAATAATG | GAATAGGACC | GCGGTTCTAT | TCTGTTGGTT | TTCGGAACTG | AGGCCATGAT | 10560 |
| TAAGAGGGAC | GGCCGGGGGC | ATTTCGTATTG | CGCCGCTAGA | GGTGAAATTC | TTGGACCGGC | 10620 |
| GCAAGACGGA | CCAGAGCGAA | AGCATTTGCC | AAGAATGTTT | TCATTAAATCA | AGAACGAAAG | 10680 |
| TCGGAGGTTT | GAAGACGATC | AGATACCGTC | GTAGTTCCGA | CCATAAACGA | TGCCGACTGG | 10740 |
| CGATGCGGGC | GCGTTATTCC | CATGACCCCG | CGGGCAGCTT | CCGGGAAACC | AAAGTCTTTG | 10800 |
| GGTTCCGGGG | GGAGTATGGT | TGCAAAGCTG | AAACTTAAAG | GAATTGACGG | AAGGGCACCA | 10860 |
| CCAGGAGTGG | GCCTGCGGCT | TAATTTGACT | CAACACGGGA | AACCTCACCC | GGCCCGGACA | 10920 |
| CGGACAGGAT | TGACAGATTG | ATAGCTCTTT | CTCGATTCCG | TGGGTGGTGG | TGCATGGCCG | 10980 |

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|-------------|-------------|-------------|-------------|------------|-------------|-------|
| TTCTTAGTTG | GTGGAGCGAT | TTGTCTGGTT | AATTCCGATA | ACGAACGAGA | CTCTGGCATG | 11040 |
| CTAACTAGTT | ACGCGACCCC | CGAGCGGTTCG | GCGTCCCCCA | ACTTCTTAGA | GGGACAAGTG | 11100 |
| GCGTTTCAGCC | ACCCGAGATT | GAGCAATAAC | AGGTCTGTGA | TGCCCTTAGA | TGTCCGGGGC | 11160 |
| TGCACGCGCG | CTACACTGAC | TGGCTCAGCG | TGTGCCTACC | CTGCGCCGGC | AGGCGCGGGT | 11220 |
| AACCCGTTGA | ACCCCATTCG | TGATGGGGAT | CGGGGATTGC | AATTATTCCC | CATGAACGAG | 11280 |
| GAATTCCCAG | TAAGTGCGGG | TCATAAGCTT | GCGTTGATTA | AGTCCCTGCC | CTTTGTACAC | 11340 |
| ACCGCCCGTC | GCTACTACCG | ATTGGATGGT | TTAGTGAGGC | CCTCGGATCG | GCCCCGCCGG | 11400 |
| GGTCGGCCCA | CGGCCCTGGC | GGAGCGCTGA | GAAGACGGTC | GAAGTTGACT | ATCTAGAGGA | 11460 |
| AGTAAAAGTC | GTAACAAGGT | TTCCGTAGGT | GAACCTGCGG | AAGGATCATT | AAACGGGAGA | 11520 |
| CTGTGGAGGA | GCGGCGGCGT | GGCCCGCTCT | CCCCGTCTTG | TGTGTGTCTT | CGCCGGGAGG | 11580 |
| CGCGTGCGTC | CCGGGTCCCG | TCGCCCGCGT | GTGGAGCGAG | GTGTCTGGAG | TGAGGTGAGA | 11640 |
| GAAGGGGTGG | GTGGGGTCCG | TCTGGGTCCG | TCTGGGACCG | CCTCCGATT | CCCCTCCCCC | 11700 |
| TCCCCCTCTC | CTCGTCCGGC | TCTGACCTCG | CCACCCTACC | GCGGCGGCGG | CTGCTCGCGG | 11760 |
| GCGTCTTGCC | TCTTTCCCGT | CCGGCTCTTC | CGTGTCTACG | AGGGGCGGTA | CGTCTGTACG | 11820 |
| GGTTTTTGAC | CCGTCCCGGG | GGCGTTCGGT | CGTCGGGGCG | CGCGCTTTGC | TCTCCCCGGA | 11880 |
| CCCATCCCCG | CCGCGGCTCT | GGCTTTTCTA | CGTTGGCTGG | GGCGGTTGTC | GCGTGTGGGG | 11940 |
| GGATGTGAGT | GTGCGGTGTG | GGCTCGCCCG | TCCCCGATGC | ACGCTTTTCT | GGCCTCGCGT | 12000 |
| GTCTTCCCCG | CTCCTGTCCC | GGGTACCTAG | CTGTGCGGTT | CCGGCGCGGA | GGTTTAAGGA | 12060 |
| CCCCGGGGGG | GTGCGCCTGC | CGCCCCCAGG | GTGCGGGGGC | GGTGGGGCCC | GTAGGGAAGT | 12120 |
| CCGTCGTTTC | GGCGGCTCTC | CCTCAGACTC | CATGACCCTC | CTCCCCCGC | TGCCGCCGTT | 12180 |
| CCCGAGCGCG | GGTCTGTGTG | GGGGGGTGGG | TGTCTGGAGC | CCCCTCGGGC | GCCGTGGGGG | 12240 |
| CCCGACCCGC | GCCGCCGGCT | TGCCCGATTT | CCGCGGGTCG | GTCTGTTCGG | TGCCGGTTCG | 12300 |
| GGGTTCCTCG | GTCGTTCCCG | TGTTTTTCCG | CTCCCGACCC | TTTTTTTTTC | CTCCCCCCCA | 12360 |
| CACGTGTCTC | GTTTCGTTCC | TGCTGGCCGG | CCTGAGGCTA | CCCCTCGGTC | CATCTGTTCT | 12420 |
| CCTCTCTCTC | CGGGGAGAGG | AGGGCGGTGG | TCGTTGGGGG | ACTGTGCCGT | CGTCAGCACC | 12480 |
| CGTGAGTTCG | CTCACACCCG | AAATACCGAT | ACGACTCTTA | GCGGTGGATC | ACTCGGCTCG | 12540 |
| TGCGTCGATG | AAGAACGCAG | CTAGCTGCGA | GAATTAATGT | GAATTGCAGG | ACACATTGAT | 12600 |
| CATCGACACT | TCGAACGCAC | TTGCGGCCCC | GGGTTCCTCC | CGGGGCTACG | CCTGTCTGAG | 12660 |
| CGTCGGTTGA | CGATCAATCG | CGTCACCCCG | TGCGGTGGGT | GCTGCGCGGC | TGGGAGTTTG | 12720 |
| CTCGCAGGGC | CAACCCCCCA | ACCCGGGTTCG | GCCCTCCGT | CTCCCGAAGT | TCAGACGTGT | 12780 |
| GGGCGGTTGT | CGGTGTGGCG | CGCGCGCCCG | CGTCGCGGAG | CCTGGTCTCC | CCCGCGCATC | 12840 |
| CGCGCTCGCG | GCTTCTTCCC | GCTCCGCCGT | TCCCGCCCTC | GCCCGTGCAC | CCCGGTCTCTG | 12900 |
| GCCTCGCGTC | GGCGCCTCCC | GGACCGCTGC | CTCACCAGTC | TTTCTCGGTC | CCGTGCCCCG | 12960 |
| TGGGAACCCA | CCGCGCCCCC | GTGGCGCCCG | GGGGTGGGCG | CGTCCGCATC | TGCTCTGGTC | 13020 |
| GAGGTTGGCG | GTTGAGGGTG | TGCGTGCGCC | GAGGTGGTGG | TCGGTCCCTT | GCGGCCGCGG | 13080 |
| GGTTGTTCGG | GTGGCGGTTCG | ACGAGGGCCG | GTCGGTTCGC | TGCGGTGGTT | GTCTGTGTGT | 13140 |
| GTTTGGGTCT | TGCGCTGGGG | GAGGCGGGGT | CGACCGCTCG | CGGGGTGGGC | GCGGTGCGCC | 13200 |
| GGCGCCGCGC | ACCTTCCGGC | TTGTGTGGAG | GGAGAGCGAG | GGCGAGAACC | GAGAGAGGTG | 13260 |
| GATATCCCGG | TGGCGTTGCG | AGGGAGGGTT | TGGCGTCCCG | CGTCCGTCCG | TCCCTCCCTC | 13320 |
| CCTCGGTGGG | CGCCTTCGCG | CCGCACGCGG | CCGCTAGGGG | CGGTGCGGGC | CCGTGGCCCC | 13380 |
| CGTGGCTCTT | CTTCGTCTCC | GCTTCTCCTT | CACCCGGGCG | GTACCCGCTC | CGGCGCCGGC | 13440 |
| CCGCGGGACG | CCGCGGCGTC | CGTGCGCCGA | TGCGAGTCAC | CCCCGGGTGT | TGCGAGTTCG | 13500 |
| GGGAGGGAGA | GGGCCCTCGT | GACCCGTTGC | GTCCCGGCTT | CCCTGGGGGG | GACCCGGCGT | 13560 |
| CTGTGGGCTG | TGCTTCCCGG | GGGTGCGTGC | TGAGTAAGAT | CCTCCACCCC | GCCGCGCCTC | 13620 |
| CCCTCCCGCC | GGCCTCTCGG | GGACCCCTTG | AGACGGTTTCG | CCGGCTCGTC | CTCCCGTGCC | 13680 |
| GCCGGGTGCC | GTCTCTTTCC | CGCCCGCCTC | CTCGCTCTCT | TCTTCCCGCG | GCTGGGCGCG | 13740 |
| TGTCCCCCCT | TTCTGACCGC | GACCTCAGAT | CAGACGTGGC | GACCCGCTGA | ATTTAAGCAT | 13800 |
| ATAGTCAGC | GGAGGAAAAG | AAACTAACCA | GGATTCCCTC | AGTAACGGCG | AGTGAACAGG | 13860 |
| GAAGAGCCCA | GCGCCGAATC | CCGCGCGCGC | GTGCGGGCGT | GGGAAATGTG | GCGTACGGAA | 13920 |
| GACCCACTCC | CCGGCGCCGC | TCGTGGGGGG | CCCAAGTCCT | TCTGATCGAG | GCCCAGCCCC | 13980 |
| TGGACGCTGT | GAGGCCGGTA | GCGGCCCGCG | CGCGCCGGGC | TCGGGTCTTC | CCGGAGTCGG | 14040 |
| GTTGCTTGGG | AATGCAGCCC | AAAGCGGGTG | GTAAACTCCA | TCTAAGGCTA | AATACCGGCA | 14100 |
| CGAGACCGAT | AGTCAACAAG | TACCGTAAGG | GAAAGTTGAA | AAGAACTTTG | AAGAGAGAGT | 14160 |
| TCAAGAGGGC | GTGAAACCGT | TAAGAGGTAA | ACGGGTGGGG | TCCGCGCAGT | CCGCCCGGAG | 14220 |
| GATTCAACCC | GGCGGCGCGC | GTCCGGCCGT | GCCCGGTGGT | CCCGGCGGAT | CTTTCCCGCT | 14280 |
| CCCCGTTCCT | CCCGACCCCT | CCACCCGCGC | GTCGTTCCCC | TCTTCTCTCC | CGCGTCCGGC | 14340 |
| GCCTCCGGCG | GCGGGCGCGG | GGGGTGGTGT | GGTGGTGGCG | GCGGGGCGGG | GCCGGGGGTT | 14400 |
| GGGTCCGGCG | GGGACCGCCC | CCGGCCGCGT | ACCGGCGGCC | GCCGGGCGCA | CTTCCACCGT | 14460 |
| GGCGGTGCGC | CGCGACCGGC | TCCGGGACGG | CCGGGAAGGC | CCGGTGGGGA | AGGTGGCTCG | 14520 |
| GGGGGGGCGG | CGCGTCTCAG | GGCGCGCCGA | ACCACCTCAC | CCCGAGTGTT | ACAGCCCTCC | 14580 |
| GGCCGCGCTT | TCGCCGAATC | CCGGGGCCGA | GGAAGCCAGA | TACCCGTGCG | CGCGCTCTCC | 14640 |
| CTCTCCCCCC | GTCCGCTTCC | CGGGCGGGCG | TGGGGTGGG | GGCCGGGCGG | CCCCTCCAC | 14700 |
| GGCGCGACCG | CTCTCCCAAC | CCCTTCCGTC | GCCTCTCTCG | GGGCCCCGGT | GGGGGCGGGG | 14760 |
| CGGACTGTCC | CCAGTGCGCC | CCGGGCGTTC | TCGCGCCGTC | GGGTCCCGGG | GGGACCGTCG | 14820 |
| GTCACGCGTC | TCCCGACGAA | GCCGAGCGCA | CGGGGTGCGC | GGCGATGTCG | GCTACCCACC | 14880 |

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|------------|------------|------------|------------|------------|------------|-------|
| CGACCCGTCT | TGAAACACGG | ACCAAGGAGT | CTAACCGGTG | CGCGAGTCAG | GGGCTCGTCC | 14940 |
| GAAAGCCGCC | GTGGCGCAAT | GAAGGTGAAG | GGCCCCGCCC | GGGGGCCCCG | GGTGGGATCC | 15000 |
| CGAGGCCTCT | CCAGTCCGCC | GAGGGCGCAC | CACCGGCCCC | TCTCGCCCCG | CGCGCCGGGG | 15060 |
| AGGTGGAGCA | CGAGCGTACG | CGTTAGGACC | CGAAAGATGG | TGAACTATGC | TTGGGCAGGG | 15120 |
| CGAAGCCAGA | GGAAACTCTG | GTGGAGGTCC | GTAGCGGTCC | TGACGTGCAA | ATCGGTCGTC | 15180 |
| CGACCTGGGT | ATAGGGGCGA | AAGACTAATC | GAACCATCTA | GTAGCTGGTT | CCCTCCGAAG | 15240 |
| TTTCCCTCAG | GATAGCTGGC | GCTCTCGCTC | CCGACGTACG | CAGTTTTATC | CGGTAAAGCG | 15300 |
| AATGATTAGA | GGTCTTGGGG | CCGAAACGAT | CTCAACCTAT | TCTCAAACCT | TAAATGGGTA | 15360 |
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| TTGGTAAGCA | GAACCTGGCG | TGCGGGATGA | ACCGAACGCC | GGGTAAAGGC | GCCCCGATGC | 15480 |
| GACGCTCATC | AGACCCCGA | AAAGGTGTTG | GTTGATATAG | ACAGCAGGAC | GGTGGCCATG | 15540 |
| GAAGTCGGAA | TCCGCTAAGG | AGTGTGTAAC | AACTCACCTG | CCGAATCAAC | TAGCCCTGAA | 15600 |
| AATGGATGGC | GCTGGAGCGT | CGGGCCCAT | CCCGGCCGTC | GCCGCAGTCG | GAACGGAACG | 15660 |
| GGACGGGAGC | GGCCGCGGGT | GCGCGTCTCT | CGGGGTCGGG | GGTGCCTGGC | GGGGGCCCGT | 15720 |
| CCCCCGCCTC | CCCTCCGCGC | GCCGGGTTCG | CCCCCGCGGC | GTCGGGCCCC | GCGGAGCCTA | 15780 |
| CGCCGCGACG | AGTAGGAGGG | CCGCTGCGGT | GAGCCTTGAA | GCCTAGGGCG | CGGGCCCGGG | 15840 |
| TGGAGCCGCC | GCAGGTGCAG | ATCTTGGTGG | TAGTAGCAAA | TATTCAAACG | AGAACTTTGA | 15900 |
| AGGCCGAAGT | GGAGAAGGGT | TCCATGTGAA | CAGCAGTTGA | ACATGGGTCA | GTCGGTCCTG | 15960 |
| AGAGATGGGC | GAGTGCCGTT | CCGAAGGGAC | GGGCGATGGC | CTCCGTTGCC | CTCGGCCGAT | 16020 |
| CGAAAGGGAG | TCCGGTTCAG | ATCCCCGAAT | CCGGAGTGGC | GGAGATGGGC | GCCGCGAGGC | 16080 |
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| TTTCTTTGTG | AAGGGCAGGG | CGCCCTGGAA | TGGGTTTCGC | CCGAGAGAGG | GGCCCGTGCC | 16200 |
| TTGGAAGCG | TCGCGGTTCC | GGCGGCGTCC | GGTGAGCTCT | CGCTGGCCCT | TGAAAATCCG | 16260 |
| GGGGAGAGGG | TGTAAATCTC | GCGCCGGGCC | GTACCCATAT | CCGCAGCAGG | TCTCCAAGGT | 16320 |
| GAACAGCCTC | TGGCATGTTG | GAACAATGTA | GGTAAGGGAA | GTCGGCAAGC | CGGATCCGTA | 16380 |
| ACTTCGGGAT | AAGGATTGGC | TCTAAGGGCT | GGGTCCGGTC | GGCTGGGGCG | CGAAGCGGGG | 16440 |
| CTGGGCGCGC | GCCGCGGCTG | GACGAGGCGC | CGCCGCCCTC | TCCCACGTCC | GGGGAGACCC | 16500 |
| CCCGTCTTTT | CCGCCCAGGC | CCGCCCTCCC | CTCTTCCCCG | CGGGGCCCCG | TCGTCCCCCG | 16560 |
| CGTCGTCGCC | ACCTCTCTTC | CCCCCTCCTT | CTTCCCGTCG | GGGGGCGGGT | CGGGGGTCGG | 16620 |
| CGCGCGGCGC | GGGCTCCGGG | GCGGCGGGTC | CAACCCCGCG | GGGGTTCGGG | AGCGGGAGGA | 16680 |
| ACCAGCGGTC | CCCGGTGGGG | CGGGGGGGCC | GGACACTCGG | GGGGCCGGCG | GCGGCGGCGA | 16740 |
| CTCTGGACGC | GAGCCGGGCC | CTTCCCCTGG | ATCGCCTCAG | CTGCGGCGGG | CGTCGCGGCC | 16800 |
| GCTCCCGGGG | AGCCCAGGCG | GTGCCGCGCG | GGGTCCCCCT | CCCGCGGGGC | CTCGCTCCAC | 16860 |
| CCCCCATCTG | CCTCTCCCGA | GGTGCGTGCG | GGGGGCGGGG | GGGCGTGTCC | CGCGCGTGTG | 16920 |
| GGGGGAACCT | CCGCTCCCGT | GTTCGCCCGC | GGGTCCGCCG | CCCCGGGCCG | CGGTTTTCCG | 16980 |
| CGCGGCGCCC | CCGCCTCGGC | CGGCGCCTAG | CAGCCGACTT | AGAAGTGGTG | CGGACCAGGG | 17040 |
| GAATCCGACT | GTTTAATTAA | AACAAAGCAT | CGCGAAGGCC | CGCGGCGGGT | GTTGACGCGA | 17100 |
| TGTGATTTCT | GCCCAGTGCT | CTGAATGTCA | AAGTGAAGAA | ATTCAATGAA | GCGCGGGTAA | 17160 |
| ACGGCGGGAG | TAACTATGAC | TCTCTTAAGC | TAGCCAAATG | CCTCGTCATC | TAATTAGTGA | 17220 |
| CGCGCATGAA | TGGATGAACG | AGATTTCCAC | TGTCTCTACC | TACTATCCAG | CGAAACACCA | 17280 |
| GCCAAGGGAA | CGGGCTTGGC | GGAATCAGCG | GGGAAAGAAG | ACCCTGTTGA | GCTTGACTCT | 17340 |
| AGTCTGGCAC | GGTGAAGAGA | CATGAGAGGT | GTAGAATAAG | TGGGAGGCCC | CCGGCGCCCC | 17400 |
| GCCCCGTCTT | CGCGTCGGGG | TCGGGGCAGC | CCGGCCTCGC | GGGCCGCGCG | TGAAATACCA | 17460 |
| CTACTCTGAT | CGTTTTTTCA | CTGACCCGGT | GAGGCGGGGG | GGCGAGCCCC | GAGGGGCTCT | 17520 |
| CGCTTCTGGC | GCCAAGCGTC | CGTCCCAGCG | GTGCGGGCGG | GCGCGACCCG | CTCCGGGGAC | 17580 |
| AGTGCCAGGT | GGGGAGTTTG | ACTGGGGCGG | TACACCTGTC | AAACGGTAAC | GCAGGTGTCC | 17640 |
| TAAGGCGAGC | TCAGGGAGGA | CAGAAACCTC | CCGTGGAGCA | GAAGGGCAAA | AGCTCGCTTG | 17700 |
| ATCTTGATTT | TCAGTACGAA | TACAGACCGT | GAAAGCGGGG | CCTCACGATC | CTTCTGACCT | 17760 |
| TTTGGGTTTT | AAGCAGGAGG | TGTCAGAAAA | GTTACCACAG | GGATAACTGG | CTTGTGGCGG | 17820 |
| CCAAGCGTTC | ATAGCGACGT | CGCTTTTTGA | TCCTTCGATG | TCGGCTCTTC | CTATCATTTG | 17880 |
| GAAGCAGAAT | TCACCAAGCG | TTGGATTGTT | CACCCACTAA | TAGGGAACGT | GAGCTGGGTT | 17940 |
| TAGACCGTCG | TGAGACAGGT | TAGTTTTTAC | CTACTGATGA | TGTGTTGTTG | CCATGGTAAT | 18000 |
| CCTGCTCAGT | ACGAGAGGAA | CCGAGGTTTC | AGACATTTGG | TGTATGTGCT | TGGCTGAGGA | 18060 |
| GCCAATGGGG | CGAAGCTACC | ATCTGTGGGA | TTATGACTGA | ACGCCTCTAA | GTCAGAAATC | 18120 |
| GCCCAAGCGG | AACGATACGG | CAGCGCCGAA | GGAGCCTCGG | TTGGCCCCCG | ATAGCCGGGT | 18180 |
| CCCCGTCCGT | CCCGCTCGGC | GGGGTCCCCG | CGTCGCCCCG | CGGCGGCGCG | GGGTCTCCCC | 18240 |
| CCGCCGGGCG | TCGGGACCGG | GGTCCGGTGC | GGAGAGCCGT | TCGTCTTGGG | AAACGGGGTG | 18300 |
| CGGCCGGAAA | GGGGGCCGCC | CTCTCGCCCG | TCACGTTGAA | CGCACGTTTC | TGTGGAACCT | 18360 |
| GGCGCTAAAC | CATTCGTAGA | CGACCTGCTT | CTGGGTGCGG | GTTTCGTACG | TAGCAGAGCA | 18420 |
| GCTCCCTCGC | TGCGATCTAT | TGAAAGTCAG | CCCTCGACAC | AAGGGTTTGT | CTCTGCGGGC | 18480 |
| TTTCCCGTCC | CACGCCCGCT | CGCTCGCACG | CGACCGTGTC | GCCGCCCCGG | CGTCACGGGG | 18540 |
| CGGGTCGCTC | CGGCCCCCGC | GCGGTTGCCG | GAACGACCGT | GTGGTGGTTG | GGGGGGGGAT | 18600 |
| CGTCTTCTCC | TCCGCTTCCC | GAGGACGGTT | GAGTTCTCTT | TCCCCCTTCC | TCGGTCTCCT | 18660 |
| TGGGTGTGGG | AGCCTCGTGC | CGTCGCGACC | GCGGCCTGCC | GTCGCTGCCG | GCCGCAGCCC | 18720 |
| CTTGCCCTCC | GGCCTTGGCC | AAGCCGGAGG | GCGGAGGAGG | GGGATCGGCG | GCGGCGGCGA | 18780 |

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GAGGGGTGGG GTGGGGGCGAG GGATCTGCAT GTCTTCTTGC AGGTCTGTGA ACTATTTGCG 22020
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TACCTGAAGT CCCTGAGTGA TGATTTCCCT GTGAATTC 22118

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | | | | | | |
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| GCTGACACGC | TGTCCTCTGG | CGACCTGTCTG | TCGAGAGAGGT | TGGGCCTCCG | GATGCGCGCG | 60 |
| GGGCTCTGGC | CTCACGGTGA | CCGGCTAGCC | GGCCGCGCTC | CTGCCTTGAG | CCGCTTGCCG | 120 |
| CGGCCCCGGG | GCCTGTCTGT | CTCTCGCGCG | TCCGAGCGTC | CCGACTCCCG | GTGCCGGCCC | 180 |
| GGGTCCGGGT | CTCTGACCCA | CCCGGGGGCG | CCGGGTAAGG | CGGCGAGGGC | CACCGTGCCC | 240 |
| CGTGCGCTCT | CCGCTGCGGG | CGCCCCGGGG | GCCGCACAAC | CCCACCCGCT | GGCTCCGTGC | 300 |
| CGTGCGTGTC | AGGCGTTCTC | GTCTCCGCGG | GGTTGTCCGC | CGCCCCCTTC | CCGGAGTGGG | 360 |
| GGGTGGCCGG | AGCCGATCGG | CTCGCTGGCC | GGCCGGCCTC | CGCTCCCGGG | GGGCTCTTCG | 420 |
| ATCGATGTGG | TGACGTCGTG | CTCTCCCGGG | CCGGGTCCGA | GCCGCGACGG | GCGAGGGGCG | 480 |
| GACGTTCTGT | GCGAACGGGA | CCGTCTTCT | CGCTCCGCCC | GCGCGGTCCC | CTCGTCTGCT | 540 |
| CCTCTCCCCG | CCCGCCGGCC | GGCGTGTGGG | AAGGCGTGGG | GTGCGGACCC | CGGCCCGACC | 600 |
| TCGCCGTCCC | GCCCCCGGCC | TTCGCTTCGC | GGGTGCGGGC | CGGCGGGGTC | CTCTGACGCG | 660 |
| GCAGACAGCC | CTGCCTGTCT | CCTCCAGTGG | TTGTGCACTT | GCGGGCGGGC | CCCCTCCGCG | 720 |
| GCGGTGGGGG | TGCCGTCCCG | CCGGCCCGTC | GTGCTGCCCT | CTCGGGGGGG | GTTTGCAGCA | 780 |
| GCGTCGGCTC | CGCCTGGGCC | CTTGCGGTGC | TCCTGGAGCG | CTCCGGGTTG | TCCCTCAGGT | 840 |
| GCCCGAGGCC | GAACGGTGGT | GTGTCTGTTC | CGCCCCCGGC | GCCCCCTCCT | CCGGTCGCCC | 900 |
| CCGCGGTGTC | CGCGCGTGGG | TCCTGAGGGA | GCTCGTCTGG | GTGGGGTTTC | AGGCGGTTTG | 960 |
| AGTGAGACGA | GACGAGACGC | GCCCCCTCCA | CGCGGGGAAG | GGCGCCCGCC | TGCTCTCGGT | 1020 |
| GAGCGCACGT | CCCGTGCTCC | CCTCTGGCGG | GTGCGCGCGG | GCCGTGTGAG | CGATCGCGGT | 1080 |
| GGGTTCGGGC | CGGTGTGACG | CGTGCGCCCG | CCGGCCGCGG | AGGGGCTGCC | GTTCTGCCTC | 1140 |
| CGACCGGTCT | TGTGTGGGTT | GACTTCGGAG | GCGCTCTGCC | TCGGAAGGAA | GGAGGTGGGT | 1200 |
| GGACGGGGGG | GCCTGGTGGG | GTGCGCGCA | CGCGCGCACC | GGCCGGGCCC | CCGCCCTGAA | 1260 |
| CGCGAACGCT | CGAGGTGGCC | GCGCGCAGGT | GTTTCCTCGT | ACCGCAGGGC | CCCCTCCCTT | 1320 |
| CCCCAGGCGT | CCCTCGGCGC | CTCTGCGGGC | CCGAGGAGGA | GCGGCTGGCG | GGTGGGGGGA | 1380 |
| GTGTGACCCA | CCCTCGGTGA | GAAAAGCCTT | CTCTAGCGAT | CTGAGAGGCG | TGCTTTGGGG | 1440 |
| GTACCGGATC | CCCCGGGGCC | CCGCCCTCTG | CTCTGCCTCC | GTTATGGTAG | CGCTGCCGTA | 1500 |
| GCGACCCGCT | CGCAGAGGAC | CCTCCTCCCG | TTCCCCCTCG | ACGGGGTTGG | GGGGGAGAAG | 1560 |
| CGAGGGTTCC | GCCGGCCACC | GCGGTGGTGG | CCGAGTTCGG | CTCGTCGCCT | ACTGTGGCCC | 1620 |
| GCGCCTCCCC | CTTCCGAGTC | GGGGGAGGAT | CCCGCCGGGC | CGGGCCCGGC | GCTCCCACCC | 1680 |
| AGCGGGTTGG | GACGCGGCGG | CCGGCGGGCG | GTGGGTGTGC | GCGCCCGGCG | CTCTGTCCCG | 1740 |
| CGCGTGACCC | CCTCCGTCCG | CGAGTCGGCT | CTCCGCCCCG | TCCCGTGCCG | AGTCGTGACC | 1800 |
| GGTGCCGACG | ACCGCGTTTG | CGTGGCACGG | GGTCGGGCCC | GCCTGGCCCT | GGGAAAGCGT | 1860 |
| CCCACGGTGG | GGGCGCGCCG | GTCTCCCGGA | GCGGGACCGG | GTCGGAGGAT | GGACGAGAAT | 1920 |
| CACGAGCGAC | GGTGGTGGTG | GCGTGTCCGG | TTCTGTGGCT | CGGTCTGCTC | GGGGCCCCCG | 1980 |
| GTGGCGGGGC | CCCGGGGGCT | GCGAGGCGGT | TCTCGGTGGG | GGCCGAGGGC | CGTCCGCGCT | 2040 |
| CCCAGCCGGG | GCGCCGCGGG | ACCGCCCTCG | TGTCTGTGGC | GGTGGGATCC | CGCGGCCGTG | 2100 |
| TTTTCCTGGT | GGCCCGGCCG | TGCTGAGGT | TTCTCCCCGA | GCCGCGCCCT | CTGCGCCGTC | 2160 |
| CCGGGTGCCC | TTGCCCTCGC | GGTCCCCGGC | CCTCGCCCGT | CTGTGCCCTC | TTCCCCGCCC | 2220 |
| GCCGCCCCCG | GATCCTCTTC | TTCCCCCCGA | GCGGCTCACC | GGCTTCACGT | CCGTTGGTGG | 2280 |
| CCCCCGCTGG | GACCGAACCC | GGCACCGCCT | CGTGGGGCGC | CGCCGCCGGC | CACTGATCGG | 2340 |
| CCCCGGCTTC | GCGTCCCCCG | GCGCGCGCCT | TGGGGACCGG | GTCGGTGGCG | CGCCGCGTGG | 2400 |
| GGCCCGGTGG | GCTTCCCGGA | GGGTTCGGGG | GGTCGGCCTG | CGGCGCGTGC | GGGGGAGGAG | 2460 |
| ACGGTTCCGG | GGGACCGGCC | GCGGCTGCGG | CGGCGGCGGT | GGTGGGGGGA | GCCGCGGGGA | 2520 |
| TCGCCGAGGG | CCGCTCGGCC | GCCCCGGGTG | CCCCGCGGTC | CCGCCGGCGG | CGGTGAGGCC | 2580 |
| CCGCGCGTGT | GTCCCCGGTG | CGGTTCGGCG | CGCTCGAGGG | GTCCCCGTGG | CGTCCCCCTC | 2640 |
| CCCGCCGGCC | GCCTTTCTCG | CGCCTTCCCC | GTCGCCCCGG | CCTCGCCCGT | GGTCTCTCGT | 2700 |
| CTTCTCCCGG | CCCGCTCTTC | CGAACCGGGT | CGGCGCGTCC | CCCGGGTGCG | CCTCGCTTCC | 2760 |
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| CGTCTCCCCC | GCGTGGCGTC | GCCCCGTTCG | GCGCGCGCGT | GCGCCCCGAG | GCGGCCCGGT | 2880 |
| GGTCCCTCCC | GGACAGGCGT | TCGTGCGACG | TGTGGCGTGG | GTCGACCTCC | GCCTTGCCGG | 2940 |
| TCGCTCGCCC | TCTCCCCGGG | TCGGGGGGTG | GGGCCCCGGG | CGGGGCCCTC | GCCCCGGTCG | 3000 |
| CTGCCTCCCC | TCCCGGGCGG | GGGCGGGCGC | GCCGGCCGGC | CTCGGTCTGC | CTCCCTTGGC | 3060 |
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| TCGGCCGGGC | CCCGGGCCCT | CGACCGGACC | GGTTCGCGCT | GCGCTGCGGC | CGCACGGCGC | 3180 |
| GACTGTCCCC | GGGCCGGGCA | CCGCGGTCCG | CCTCTCGCTC | GCCGCCCGGA | CGTCGGGGCC | 3240 |
| GCCCCGCGGG | GCGGGCGGAG | CGCCGTCCCC | GCCTCGCCGC | CGCCCCGCGG | CGCCGGCCGC | 3300 |
| GCGCGCGCGC | GCGTGGCCGC | CGGTCCCTCC | CGGCCCGCGG | GCGCGGGTCG | GGCCGTCCGC | 3360 |
| CTCCTCGCGG | GCGGGCGCGA | CGAAGAAGCG | TCGCGGGTCT | GTGGCGCGGG | GCCCCCGGTG | 3420 |

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| GTCGTGTCGC | GTGGGGGGCG | GGTGGTTGGG | GCGTCCGGTT | CGCCGCGCCC | CGCCCCGGCC | 3480 |
| CCACCGGTCC | CGGCCGCGCC | CCCCGCGCCC | GCTCGCTCCC | TCCCGTCCGC | CCGTCCGCGG | 3540 |
| CCCGTCCGTC | CGTCCGTCCG | TCGTCTCTCT | CGCTTGCGGG | GCGCCGGGGC | CGTCTCTCGC | 3600 |
| AGGCCCCCGG | GCCGGCCGTC | CGGCCGCGTC | GGGGGCTCGC | CGCGCTCTAC | CTTACCTACC | 3660 |
| TGGTTGATCC | TGCCAGTAGC | ATATGCTTGT | CTCAAAGATT | AAGCCATGCA | TGTCTAAGTA | 3720 |
| CGCACGGCCG | GTACAGTGAA | ACTGCGAATG | GCTCATTAAA | TCAGTTATGG | TTCCTTTGGT | 3780 |
| CGCTCGCTCC | TCTCTACTTT | GGATAACTGT | GGTAATTCTA | GAGCTAATAC | ATGCCGACGG | 3840 |
| GCGCTGACCC | CCTTCGCGGG | GGGGATGCGT | GCATTTATCA | GATCAAAAACC | AACCCGGTCA | 3900 |
| GCCCCCTCTC | GGCCCCGGCC | GGGGGGCGGG | CGCCGGCGGC | TTTGGTGAAT | CTAGATAACC | 3960 |
| TCGGGGCCGAT | CGCACGCCCC | CCGTGGCGGC | GACGACCCAT | TCGAACGTCT | GCCCTATCAA | 4020 |
| CTTTTCGATGG | TAGTCGCCGT | GCCTACCATG | GTGACCACGG | GTGACGGGGA | ATCAGGGTTC | 4080 |
| GATTCCGGAG | AGGGAGCCTG | AGAAACGGCT | ACCACATCCA | AGGAAGGCAG | CAGGCGCGCA | 4140 |
| AATTACCCAC | TCCCGACCCG | GGGAGGTAGT | GACGAAAAAT | AACAATACAG | GACTCTTTTCG | 4200 |
| AGGCCCTGTA | ATTGGAATGA | GTCCACTTTA | AATCCTTTAA | CGAGGATCCA | TTGGAGGGCA | 4260 |
| AGTCTGGTGC | CAGCAGCCGC | GGTAATTCCA | GCTCCAATAG | CGTATATTAA | AGTTGCTGCA | 4320 |
| GTTAAAAAGC | TCGTAGTTGG | ATCTTGCGAG | CGGGCGGGCG | GTCCGCGCGC | AGGCGAGCCA | 4380 |
| CCGCCCCGTC | CCGCCCCCTG | CCTCTCGGCG | CCCCCTCGAT | GCTCTTAGCT | GAGTGTCCCG | 4440 |
| CGGGGCCCCG | AGCGTTTACT | TTGAAAAAAT | TAGAGTGTTT | AAAGCAGGCC | CGAGCCGCCT | 4500 |
| GGATACCGCA | GCTAGGAATA | ATGGAATAGG | ACCGCGGTTT | TATTTTGTGG | GTTTTTCGGAA | 4560 |
| CTGAGGCCAT | GATTAAGAGG | GACGGCCGGG | GGCATTTCGA | TTGCGCCGCT | AGAGGTGAAA | 4620 |
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| ACCAAAGTCT | TTGGGTTCCG | GGGGGAGTAT | GGTTGCAAAAG | CTGAAACTTA | AAGGAATTGA | 4860 |
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| ATCATTAACG | GAGCCCGGAG | GGCGAGGCC | GCGGCGGCGC | CGCCGCGGCC | GCGCGCTTCC | 5580 |
| CTCCGCACAC | CCACCCCCC | ACCGCGACGC | GGCGCGTGCG | CGGGCGGGGC | CCGCGTGCCC | 5640 |
| GTTCGTTTCG | TCGTCGTTTC | GTTTCGCCGC | CGGCCCGGCC | GCCGCGAGAG | CCGAGAACTC | 5700 |
| GGGAGGGAGA | CGGGGGGAG | AGAGAGAGAG | AGAGAGAGAG | AGAGAGAGAG | AGAGAGAGAA | 5760 |
| AGAAGGGCGT | GTCGTTGGTG | TGCGCGTGTC | GTGGGGCCGG | CGGGCGGCGG | GGAGCGGTCC | 5820 |
| CCGGCCGCGG | CCCCGACGAC | GTGGGTGTCT | GCGGGCGCGG | GGGCGGTTCT | CGGCGGCGTC | 5880 |
| GCGGCGGGTC | TGGGGGGGTC | TCCGTGCCCT | CCTCCCCGCC | GGGGCCCCGC | GTCCGGCCCC | 5940 |
| GCCGCGCCGG | CTCCCCGTCT | TCGGGGCGGG | CCGGATTCCC | GTCCGCTCCG | CCGCGCCGCT | 6000 |
| CCGCGCCGCC | GGGCACGGCC | CGGCTCGCTC | TCCCCGGCCT | TCCCGCTAGG | GCGTCTCGAG | 6060 |
| GGTCGGGGGC | CGGACGCCGG | TCCCCCTCCC | CGCCTCCTCG | TCCGCCCCCC | CGCCGTCCAG | 6120 |
| GTACCTAGCG | CGTTCCGGCG | CGGAGGTTTA | AAGACCCCTT | GGGGGGGATC | CCCGTCCGCC | 6180 |
| CCTGGGTCCG | GGGCGGTGGT | GGGCCGCGCG | GGGAGTCCCG | TCGGGAGGGG | CCCGGCCCTT | 6240 |
| CCGCGCCTTC | CACCGCGGAC | TCCGCTCCCC | GCGCGGGGCC | GCGCCGCGCG | CGCCGCGCGC | 6300 |
| GCGGCGCTCG | GGTGGGGGCT | TTACCCGGCG | GCCGTCGCGC | GCCTGCCGCG | CGTGTGGCGT | 6360 |
| GCGCCCCGCG | CCGTGGGGGC | GGGAACCCCC | GGGCGCCTGT | GGGGTGGTGT | CCGCGCTCGC | 6420 |
| CCCCGCGTGG | GCGGCGCGCG | CCTCCCCGTG | GTGTGAAACC | TTCCGACCCC | TCTCCGAGAT | 6480 |
| CCGGTCCCGT | TTGCTGTCTC | GTCTGGCCGG | CCTGAGGCAA | CCCCCTCTCC | TCTTGGGCGG | 6540 |
| GGGGGGCGGG | GGGACGTGCC | GCGCCAGGAA | GGGCTCCTCT | CCGGTGCCTG | GTCCGGAGCG | 6600 |
| CCCTCGCCAA | ATCGACCTCG | TACGACTCTT | AGCGGTGGAT | CACTCGGCTC | GTGCGTCGAT | 6660 |
| GAAGAACGCA | GCTAGCTGCG | AGAATTAATG | TGAATTGCAG | GACACATTGA | TCATCGACAC | 6720 |
| TTCGAACGCA | CTTGCGGGCC | CGGGTTCCTC | CCGGGGCTAC | GCCTGTCTGA | GCGTCCGTTG | 6780 |
| CCGATCAATC | GCCCCGGGGG | TGCCCTCCGG | CTCCTCGGGG | TGCGCGGCTG | GGGGTTCCTT | 6840 |
| GCGAGGGCCC | CCCGGGGGCC | CTCCGTCCCC | CTAAGCGCAG | ACCCGGCGGC | GTCCGCCCTC | 6900 |
| CTCTTGCCGC | CGCGCCCGCC | CCTTCCCCCT | CCCCCGCGCG | GCCCTGCGTG | GTCACGCGTC | 6960 |
| GGGTGGCGGG | GGGAGAGGGG | GGGCGCGCCC | GGCTGAGAGA | GACGGGGAGG | GCGGCGCCGC | 7020 |
| CGCCGGAAGA | CGGAGAGGGA | AAGAGAGAGC | CGGCTCGGGC | CGAGTTCCCG | TGGCCGCCGC | 7080 |
| CTGCGGTCCG | GGTTCCTCCC | TCGGGGGGCT | CCCTCGCGCC | GCGCGCGGCT | CGGGGTTCCG | 7140 |
| GGTTCGTCGG | CCCCGGCCGG | GTGGAAGGTC | CCGTGCCCCG | CGTCGTCGTC | GTCGCGCGTC | 7200 |
| GTCGGCGGTG | GGGGCGGTGT | GCGTGCGGTG | TGGTGGTGGG | GGAGGAGGAA | GCGGGTCCG | 7260 |
| GAAGGGGAAG | GGTGCCGGCG | GGGAGAGAGG | GTCGGGGGAG | CGCGTCCCGG | TCGCGCGGCT | 7320 |

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|-------------|-------------|------------|------------|------------|-------------|-------|
| TCCGCCGCC | GCCCCCGGTG | GCGGCCCGGC | GTCCGGCCGA | CCGGCCGCTC | CCCGCGCCCC | 7380 |
| TCCTCCTCCC | CGCCGCCCCT | CCTCCGAGGC | CCCGCCCGTC | CTCCTCGCCC | TCCCCGCGCG | 7440 |
| TACGCGCGCG | CGCCCGCCCC | CCCGGCTCGC | CTCGCGGCGC | GTCGGCCGGG | GCCGGGAGCC | 7500 |
| CGCCCCGCCG | CCCGCCCCGTG | GCCGCGGCGC | CGGGGTTCGC | GTGTCCCCCG | CGGCGACCCG | 7560 |
| CGGGACGCCG | CGGTGTCTGC | CGCCGTTCGC | CGCCCCCCTC | CGGCTCGCGG | CCGCGCCGCG | 7620 |
| CCGCGCCGGG | GCCCCGTCCC | GAGCTTCCGC | GTGCGGGCGG | CGCGGCTCCG | CCGCCGCGTC | 7680 |
| CTCGGACCCG | TCCCCCGAC | CTCCGCGGGG | GAGACGCGCC | GGGGCGTGCG | GCGCCCCGTC | 7740 |
| CGCCCCCGGC | CCGTGCCCTT | CCCTCCGGTC | GTCCCGCTCC | GGCGGGGCGG | CGCGGGGGCG | 7800 |
| CCGTGCGCCG | CGCGCTCTCT | CTCCCGTCGC | CTCTCCCCCT | CGCCGGGCCC | GTCTCCCGAC | 7860 |
| GGAGCGTCGG | GCGGGCGGTC | GGGCGGCGCG | GATTCCGTCC | GTCCGTCCGC | CGAGCGGCCC | 7920 |
| GTCCCCCTCC | GAGACGCGAC | CTCAGATCAG | ACGTGGCGAC | CCGCTGAATT | TAAGCATATT | 7980 |
| AGTCAGCGGA | GGAAAAGAAA | CTAACCAGGA | TTCCCTCAGT | AACGGCGAGT | GAACACGGAA | 8040 |
| GAGCCACGCG | CCGAATCCCC | GCCCCGCGGG | GCGCGGGACA | TGTGGCGTAC | GGAAGACCCG | 8100 |
| CTCCCCGCGG | CCGCTCGTGG | GGGGCCCAAG | TCCTTCTGAT | CGAGGCCAG | CCCGTGGACG | 8160 |
| GTGTGAGGCC | GGTAGCGGCC | GGCGCGCGCC | CGGGTCTTCC | CGGAGTCGGG | TTGCTTGGGA | 8220 |
| ATGCAGCCCC | AAGCGGTGG | TAAACTCCAT | CTAAGGCTAA | ATACCGGCAC | GAGACCGATA | 8280 |
| GTCAACAAGT | ACCGTAAGGG | AAAGTTGAAA | AGAAGTTTGA | AGAGAGAGTT | CAAGAGGGCG | 8340 |
| TGAAACCGTT | AAGAGGTAAA | CGGGTGGGGT | CCGCGCAGTC | CGCCCGGAGG | ATTCAACCCG | 8400 |
| GCGGCGGGTC | CGGCCGTGTC | GGCGGCCCGG | CGGATCTTTC | CCGCCCCCGG | TCCCTCCCCGA | 8460 |
| CCCCCTCCACC | CGCCCTCCCT | TCCCCCGCGC | CCCCCTCTCC | TCCTCCCCCG | AGGGGGCGGG | 8520 |
| CTCCGGCGGG | TGCGGGGGTG | GGCGGGCGGG | GGCGGAGTGT | GGGTCCGCGG | GGGACCGTCC | 8580 |
| CCCGACCGGC | GACCGGCCGC | CGCCGGGCGC | ATTTCCACCG | CGGCGGTGCG | CCGCGACCCG | 8640 |
| CTCCGGGACG | GCTGGGAAGG | CCCGGCGGGG | AAGGTGGCTC | GGGGGGCCCC | GTCCGTCCGT | 8700 |
| CCGTCTCTCT | CCTCCCCCGT | CTCCGCCCCC | CGGCCCCCGG | TCCTCCCTCG | GGAGGGCGCG | 8760 |
| CGGGTCGGGG | CGGCGGCGGC | GGCGGCGGTG | GCGGCGGCGG | CGGGGGCGGC | GGGACCGAAA | 8820 |
| CCCCCCCCGA | GTGTTACAGC | CCCCCGGCA | CGAGCACTCG | CCGAATCCCG | GGGCGGAGGG | 8880 |
| AGCGAGACCC | GTCGCCGCGC | TCTCCCCCT | CCCGGCGCCC | ACCCCGCGCG | GGAATCCCCC | 8940 |
| GCGAGGGGGG | TCTCCCCCGC | GGGGGCGCGC | CGGCGTCTCC | TCGTGGGGGG | GCCGGGCCAC | 9000 |
| CCCTCCCACG | GCGCGACCGC | TCTCCCACCC | CTCCTCCCCG | CGCCCCCGCC | CCGGCGACGG | 9060 |
| GGGGGGTGCC | GCGCGCGGGT | CGGGGGGCGG | GGCGGACTGT | CCCCAGTGCG | CCCCGGGCGG | 9120 |
| GTCGCGCCGT | CGGGCCCCGG | GGAGGTTCTC | TCGGGGCCAC | GCGCGCGTCC | CCCGAAGAGG | 9180 |
| GGGACGCGCG | AGCGAGCGCA | CGGGGTCCGC | GGCGACGTCG | GCTACCCACC | CGACCCGTCT | 9240 |
| TGAAACACGG | ACCAAGGAGT | CTAACACGTG | CGCGAGTCGG | GGGCTCGCAC | GAAAGCCGCC | 9300 |
| GTGGCGCAAT | GAAGGTGAAG | GCCGGCGCGC | TCGCGGCGCG | AGGTGGGATC | CCGAGGCCCT | 9360 |
| TCCAGTCCGC | CGAGGGCGCA | CCACCGGCCC | GTCTCGCCCG | CCGCGCCGGG | GAGGTGGAGC | 9420 |
| ACGAGCGCAC | GTGTTAGGAC | CCGAAAGATG | GTGAACTATG | CCTGGGCAGG | GCGAAGCCAG | 9480 |
| AGGAAACTCT | GGTGGAGGTC | CGTAGCGGTC | CTGACGTGCA | AATCGGTTCG | CCGACCTGGG | 9540 |
| TATAGGGGCG | AAAGACTAAT | CGAACCATCT | AGTAGCTGGT | TCCCTCCGAA | GTTTCCCTCA | 9600 |
| GGATAGCTGG | CGCTCTCGCA | GACCCGACGC | ACCCCGTGCA | CGCAGTTTTA | TCCGGTAAAG | 9660 |
| CGAATGATTA | GAGGTCTTGG | GGCCGAAACG | ATCTCAACCT | ATTCTCAAAC | TTTAAATGGG | 9720 |
| TAAGAAGCCC | GGCTCGCTGG | CGTGGAGCCG | GGCGTGGAAT | GCGAGTGCCT | AGTGGGCCAC | 9780 |
| TTTTGGTTAAG | CAGAACTGGC | GCTGCGGGAT | GAACCGAACG | CCGGGTTAAG | GCGCCCGATG | 9840 |
| CCGACGCTCA | TCAGACCCCA | GAAAAGGTGT | TGGTTGATAT | AGACAGCAGG | ACGGTGGCCA | 9900 |
| TGGAAGTCCG | AATCCGCTAA | GGAGTGTGTA | ACAACTCACC | TGCCGAATCA | ACTAGCCCTG | 9960 |
| AAAATGGATG | GCGCTGGAGC | GTCGGGCCCA | TACCCGGCCG | TCGCCGGCAG | TCGAGAGTGG | 10020 |
| ACGGGAGCGG | CGGGGGCGGC | GCGCGCGCGC | GCGCGTGTGG | TGTGCGTCCG | AGGGCGGCGG | 10080 |
| CGCGGCGCGC | GGCGGGGGTG | TGGGGTCCTT | CCCCCGCCCC | CCCCCCCCAC | CCTCCTCCCC | 10140 |
| TCCTCCCCGC | CACGCCCCCG | TCCCCGCCCC | CGGAGCCCCG | CGGACGCTAC | CCGCGGACGA | 10200 |
| GTAGGAGGGC | CGCTGCGGTG | AGCCTTGAAG | CCTAGGGCGC | GGGCCCCGGT | GGAGCCGCCG | 10260 |
| CAGGTGCAGA | TCTTGGTGGT | AGTAGCAAAT | ATTCAAACGA | GAACCTTGAA | GGCCGAAGTG | 10320 |
| GAGAAGGGTT | CCATGTGAAC | AGCAGTTGAA | CATGGGTGAG | TCGGTCTTGA | GAGATGGGCG | 10380 |
| AGCGCCGTTT | CGAAGGGACG | GGCGATGGCC | TCCGTTGCC | TCGGCCGATC | GAAAGGGAGT | 10440 |
| CGGGTTTCAG | TCCCCGAATC | CGGAGTGGCG | GAGATGGGCG | CCGCGAGGCG | TCCAGTGCGG | 10500 |
| TAACCGGACC | GATCCCGGAG | AAGCCGGCGG | GAGCCCCGGG | GAGAGTTCTC | TTTTCTTTGT | 10560 |
| GAAGGGCAGG | GCGCCCTGGA | ATGGGTTCGC | CCCGAGAGAG | GGGCCCCGTC | CTTGGAAGAG | 10620 |
| GTCGCGGTTT | CGGCGGCGTC | CGGTGAGCTC | TCGCTGGCCC | TTGAAAATCC | GGGGGAGAGG | 10680 |
| GTGTAAATCT | CGCGCCGGGC | CGTACCCATA | TCCGCAGCAG | GTCTCCAAGG | TGAACAGCCT | 10740 |
| CTGGCATGTT | GGAAACAATG | AGTAAGGGA | AGTCGGCAAG | CCGGATCCGT | AACTTCGGGA | 10800 |
| TAAGGATTGG | CTCTAAGGGC | TGGGTGCGTC | GGGCTGGGGC | GCGAAGCGGG | GCTGGGCGCG | 10860 |
| CGCCGCGGCT | GGACGAGGCG | GCGCCCCCCC | CCACGCCCCG | GGCACCCCCC | TCGCGGCCCT | 10920 |
| CCCCCGCCCC | ACCCGCGCGC | GCCGCTCGCT | CCCTCCCCAC | CCCGCGCCCT | CTCTCTCTCT | 10980 |
| CTCTCCCCCG | CTCCCCGTCC | TCCCCCTCC | CCGGGGGAGC | GCCGCGTGGG | GGCGCGGCGG | 11040 |
| GGGGAGAAGG | GTCGGGGCGG | CACGGGGCGG | CCGGGGCGCG | CCGGGGCGGC | CGGCGGGGGC | 11100 |
| AGGTCCCCGC | GAGGGGGGCC | CCGGGGACCC | GGGGGGCCGG | CGGCGGCGCG | GACTCTGGAC | 11160 |
| GCGAGCCGGG | CCCTTCCCGT | GGATCGCCCC | AGCTGCGGCG | GGCGTCGCGG | CCGCCCCCGG | 11220 |

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|------------|------------|------------|-------------|------------|-------------|-------|
| GGAGCCCGGC | GGCGGCGCGG | CGCGCCCCCC | ACCCCCACCC | CACGTCTCGG | TCGCGCGCGC | 11280 |
| GTCCGCTGGG | GGCGGGAGCG | GTCGGGCGGG | GGCGGTCTGG | GGGCGGCGGG | GCGGGGCGGT | 11340 |
| TCGTCCCCCC | GCCCTACCCC | CCCGCCCCCG | TCCGCCCCCC | GTTCCCCCCT | CCTCCTCGGC | 11400 |
| GCGCGGCGGC | GGCGGCGGCA | GGCGGCGGAG | GGGCGCGGGG | CCGGTCCCCC | CCGCGGGGTC | 11460 |
| CGCCCCCGGG | GCCGCGGTTC | CGCGCGCGCC | TCGCCTCGGC | CGGCGCCTAG | CAGCCGACTT | 11520 |
| AGAACTGGTG | CGGACCAGGG | GAATCCGACT | GTTTAATTAA | AACAAAGCAT | CGCGAAGGCC | 11580 |
| CGCGGCGGGT | GTTGACGCGA | TGTGATTTCT | GCCCAGTGCT | CTGAATGTCA | AAGTGAAGAA | 11640 |
| ATTCAATGAA | GCGCGGGTAA | ACGGCGGGAG | TAACATATGAC | TCTCTTAAGG | TAGCCAAATG | 11700 |
| CCTCGTCATC | TAATTAGTGA | CGCGCATGAA | TGGATGAACG | AGATTCCCAC | TGTCCCTACC | 11760 |
| TACTATCCAG | CGAAACCACA | GCCAAGGGAA | CGGGCTTGGC | GGAATCAGCG | GGGAAAGAAG | 11820 |
| ACCCTGTTGA | GCTTGACTCT | AGTCTGGCAC | GGTGAAGAGA | CATGAGAGGT | GTAAGAATAAG | 11880 |
| TGGGAGGCC | CCGGCGCCCC | CCCGGTGTCC | CCGCGAGGGG | CCCGGGGCGG | GGTCCGCGGC | 11940 |
| CCTGCGGGCC | GCCGGTGAAA | TACCACTACT | CTGATCGTTT | TTTCACTGAC | CCGGTGAGGC | 12000 |
| GGGGGGGCGA | GCCCGAGGGG | CTCTCGCTTC | TGGCGCCAAG | CGCCCGCCCC | GCCGGGCGCG | 12060 |
| ACCCGCTCCG | GGGACAGTGC | CAGGTGGGGA | GTTTGACTGG | GGCGGTACAC | CTGTCAAACG | 12120 |
| GTAACGCAGG | TGTCCTAAGG | CGAGCTCAGG | GAGGACAGAA | ACCTCCCGTG | GAGCAGAAGG | 12180 |
| GCAAAAGCTC | GCTTTGATCT | GATTTTCAGT | ACGAATACAG | ACCGTGAAAG | CGGGGCCTCA | 12240 |
| CGATCCTTCT | GACCTTTTGG | GTTTTAAGCA | GGAGGTGTCA | GAAAAGTTAC | CACAGGGATA | 12300 |
| ACTGGCTTGT | GGCGGCCAAG | CGTTCATAGC | GACGTGCTTT | TTTGATCCTT | CGATGTCGGC | 12360 |
| TCTTCCTATC | ATTGTGAAGC | AGAATTCGCG | AAGCGTTGGA | TTGTTACCCC | ACTAATAGGG | 12420 |
| AACGTAGACT | GGTTTTAGAC | CGTCGTGAGA | CAGGTTAGTT | TTACCCTACT | GATGATGTGT | 12480 |
| TGTTGCCATG | GTAATCCTGC | TCAGTACGAG | AGGAACCGCA | GGTTCAGACA | TTTGGTGTAT | 12540 |
| GTGCTTGGCT | GAGGAGCCAA | TGGGGCGAAG | CTACCATCTG | TGGGATTATG | ACTGAACGCC | 12600 |
| TCTAAGTCAG | AATCCCGCCC | AGGCGAACGA | TACGGCAGCG | CCGCGGAGCC | TCGGTTGGCC | 12660 |
| TCGGATAGCC | GGTCCCCCGC | CTGTCCCCCG | CGGCGGGCCG | CCCCCCCCCT | CACGCGCCCC | 12720 |
| GCCGCGGGAG | GCGCGGTGCC | CCGCGCGCGC | CCGGGACCCG | GGTCCGGTGC | GGAGTGCCCT | 12780 |
| TCGTCTCGGG | AAACGGGGCG | CGGCCGGAAA | GGCGGCCGCC | CCCTCGCCCC | TCACGCACCG | 12840 |
| CACGTTCGTG | GGGAACCTGG | CGCTAAACCA | TTCTGTAGAC | ACCTGCTTCT | GGGTGCGGGT | 12900 |
| TTCGTACGTA | GCAGAGCAGC | TCCCTCGCTG | CGATCTATTG | AAAGTCAGCC | CTCGACACAA | 12960 |
| GGGTTTGTTC | GCGCGCGCGT | GCGTGCGGGG | GGCCCGCGCG | GCGTGCGCGT | TCGGCGCCGT | 13020 |
| CCGTCTTTC | GTTTCGTCTT | CTCCCTCCCC | GCCTCTCCCC | CCGACCGCGG | CGTGGTGGTG | 13080 |
| GGGTGGGGGG | GAGGGCGCGC | GACCCCGGTC | GGCCGCCCCG | CTTCTTCGGT | TCCCGCCTCC | 13140 |
| TCCCCGTTCA | CGCCGGGGCG | GCTCGTCCGC | TCCGGGCCGG | GACGGGGTCC | GGGGAGCGTG | 13200 |
| GTTTGGGAGC | CGCGGAGGCG | CCGCGCCGAG | CCGGCCCCCG | TGGCCCCCGC | GTCCCCGTCC | 13260 |
| CGGGGGTTGG | CCGCGCGGGC | CGGTGGGGGG | CCACCCGGGG | TCCCGGCCCT | CGCGCGTCC | 13320 |
| TCCTCTCTCG | TCCTCCGCAC | GGGTGACCG | ACGAACCGCG | GGTGGCGGGC | GGCGGGCGGC | 13380 |
| GAGCCCCACG | GGCGTCCCCG | CACCCGGCCG | ACCTCCGCTC | GCGACCTCTC | CTCGGTGCGG | 13440 |
| CCTCCGGGAT | CGACCGCCTG | CGCCCGCGGG | CGTGAGACTC | AGCGGCGTCT | CGCCGTGTCC | 13500 |
| GCGTCTGCGT | GCGGCTCTCT | CCACGAGCG | CGGGTGTAGG | AGTGCCCGTC | GGGACGAACC | 13560 |
| GCAACCGGAG | CGTCCCCGTC | TCGGTCGGCA | CCTCCGGGGT | CGACCAGCTG | CCGCCCCGCA | 13620 |
| GCTCCGGACT | TAGCCGGCGT | CTGCACGTGT | CCCGGGTCGA | CCAGCAGGCG | GCCGCCGGAC | 13680 |
| GCAGCGGCGC | ACGCACGCGA | GGGCGTCGAT | TCCCCTTTCG | GCGCCCCGCG | CTCCACCGGC | 13740 |
| CTCGGCCCCG | GGTGGAGCTG | GGACCACGCG | GAACCTCCCT | TCCCACATTT | TTTTACAGCC | 13800 |
| CACCGCGAGT | TTGCGTCCGC | GGGACCTTTA | AGAGGGAGTC | ACTGCTGCCG | TCAGCCAGTA | 13860 |
| CTGCCTCCTC | CTTTTTTCGT | TTTAGGTTTT | GCTTGCCTTT | TTTTTTTTTT | TTTTTTTTTT | 13920 |
| TTTTTTCTTT | CTTTCTTTCT | TTCTTTCTTT | CTTTCTTTCT | TTCTTTCTTT | CGCTTGTCTT | 13980 |
| CTTCTTGTGT | TCCTTCTTGT | CTCTTCTCT | GTCTGTCTCT | CTCTCTCTCT | CTCTCTCTGT | 14040 |
| CTCTCGTCTG | TCCTTCTCT | CTCTTCTCT | TCTCTCTCT | TCTCTCTCT | TCTCTCGCTC | 14100 |
| TCGCCCTCTC | TCTCTCTCT | CTCTCTGTCT | CTCTCTCTCT | CTCTCTCTCT | CTCTCTCTCT | 14160 |
| GTCGCTCTCG | CCCTCTCGCT | CTCTCTCTGT | CTCTGTCTGT | GTCTCTCTCT | CTCCCTCCCT | 14220 |
| CCCTCCCTCC | CTCCCTCCCT | CCCTCCCTCT | CCTTGGCGCC | TTCTCGGCTC | TTGAGACTTA | 14280 |
| GCCGCTGTCT | CGCCGTACCC | CGGGTCGACC | GGCGGGCCCT | CTCCACCGAG | CGGCGTGCCA | 14340 |
| CAGTGCCCGT | CGGGACGAGC | CGGACCCGCC | GCGTCCCCGT | CTCGGTGCGG | ACCTCCGGGG | 14400 |
| TCGACCAGCT | GCCGCCCGCG | AGCTCCGGAC | TTAGCCGGCG | TCTGCACGTG | TCCCGGGTCG | 14460 |
| ACCAGCAGGC | GGCCGCCCGA | CGCAGCGGCG | CACCGACGGA | GGGCGCTGAT | TCCCGTTCAC | 14520 |
| GCGCCCCGCG | CTCCACCGGC | CTCGGCCCGC | CGTGGAGCTG | GGACCACGCG | GAACCTCCCT | 14580 |
| TCCTACATTT | TTTTACAGCC | CACCGCAGGT | TTGCGTCCCG | GGGACCTTTA | AGAGGGAGTC | 14640 |
| ACTGCTGCCG | TCAGCCAGTA | CTGCCTCCTC | CTTTTTCGCT | TTTAGGTTTT | GCTTGCCTTT | 14700 |
| TTTTTTTTTT | TTTTTTTTTT | TTTTTTCTTT | CTTTCTTTCT | TTCTTTCTTT | CTTTCTTTCT | 14760 |
| TTCTTTCTTT | CTTTCTCTCT | CGCTCTCTCG | CTCTCTCCCT | CGCTCGTTTC | TTTCTTTCTC | 14820 |
| TTTCTCTCTC | TCTCTCTCTC | TCTCTCTCTC | TCTGTCTCTC | GCTCTCGCCC | TCTCTCTCTC | 14880 |
| TTTCTCTCTC | TCTCTCTCTC | TCTCTCTCTC | TCTCTCTCTC | TCTCTCTCTC | CCTCCTCCTC | 14940 |
| TCCCCCTCCC | TCCCTCTCTC | CCCTTCCTTG | GCGCCTTCTC | GGCTCTTGAG | ACTTAGCCGC | 15000 |
| TGTCTCGCCG | TGTCCCGGGT | CGACCGGCGG | GCCTTCTCCA | CCGAGCGGCG | TGCCACAGTG | 15060 |
| CCCGTCGGGA | CGAGCCGGAC | CCGCCGCGTC | CCCGTCTCGG | TCGGCACCTC | CGGGGTGCGC | 15120 |

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|-------------|------------|-------------|-------------|-------------|-------------|-------|
| CAGCTGCCGC | CCGCGAGCTC | CGGACTTAGC | CGGCGTCTGC | ACGTGTCCCG | GGTCGACCAG | 15180 |
| CAGGCGGCCG | CCGGACGCTG | CGGCGCACC | ACGCGAGGGC | GTCGATTCCG | GTTACGCGC | 15240 |
| CGGCGACCTC | CACCGGCCTC | GGCCCGCGGT | GGAGCTGGGA | CCACGCGGAA | CTCCCTCTCC | 15300 |
| CACATTTTTT | TCAGCCCCAC | CGCGAGTTTG | CGTCCGCGGG | ACTTTTAAGA | GGGAGTCACT | 15360 |
| GCTGCCGTCA | GCCAGTAATG | CTTCCTCTCT | TTTTGCTTTT | TGGTTTTGCC | TTGCGTTTTC | 15420 |
| TTTCTTTCTT | TCTTTCTTTC | TTTCTTTCTT | TCTTTCTTTC | TCTCTCTCTC | TCTCTCTCTC | 15480 |
| TCTCTGTCTC | TCTCTCTCTG | TCTCTCTCCC | CTCCCTCCCT | CCTTGGTGCC | TTCTCGGCTC | 15540 |
| GCTGTGCTG | CTGCCTCTGC | CTCCACGGTT | CAAGCAAACA | GCAAGTTTTT | TATTTTCGAGT | 15600 |
| AAAGACGTAA | TTTCACCATT | TTGGCCGGGC | TGGTCTCGAA | CTCCCGACCT | AGTGATCCGC | 15660 |
| CCGCCTCGGC | CTCCCAAAGA | CTGCTGGGAG | TACAGATGTG | AGCCACCATG | CCCGGCCGAT | 15720 |
| TCCTTCCTTT | TTTCAATCTT | ATTTTCTGAA | CGCTGCCCGT | TATGAACATA | CATCTACACA | 15780 |
| CACACACACA | CACACACACA | CACACACACA | CACACACACA | CACACACCCC | GTAGTGATAA | 15840 |
| AACTATGTAA | ATGATATTTT | CATAATTAAT | ACGTTTATAT | TATGTTACTT | TTAATGGATG | 15900 |
| AATATGTATC | GAAGCCCCAT | TTCATTTACA | TACACGTGTA | TGTATATCCT | TCCTCCCTTC | 15960 |
| CTTCATTCA | TATTTATTAA | TAATTTTCGT | TTATTTATTT | TCTTTTCTTT | TGGGGCCCGC | 16020 |
| CCGCCTGGTC | TTCTGTCTCT | GCGCTCTGGT | GACCTCAGCC | TCCCAAATAG | CTGGGACTAC | 16080 |
| AGGGATCTCT | TAAGCCCGGG | AGGAGAGGTT | AACGTGGGCT | GTGATCGCAC | ACTTCCACTC | 16140 |
| CAGCTTACGT | GGGCTGCGGT | GCGGTGGGGT | GGGGTGGGGT | GGGGTGGGGT | GCAGAGAAAA | 16200 |
| CGATTGATTG | CGATCTCAAT | TGCCCTTTTAG | CTTCATTCA | ACCCTGTTAT | TTGCTCGTTT | 16260 |
| ATTCTCATGG | GTTCTTCTGT | GTCATTGTCA | CGTTTATCTG | TTGCTTGCCT | GCTTGCCTGT | 16320 |
| TTATTTCTTT | CCTTCTTCTC | TTCTTCTTCC | CCTTCTTCTC | TTCTTCTTCC | CCCTCCCTTA | 16380 |
| CTGGCAGGGT | CTTCTCTCTG | CTCTGCGGCC | CAGGATCACC | CCAACCTCAA | CGCTTTGGAC | 16440 |
| CGACCAAACG | GTCGTTCTGC | CTCTGATCCC | TCCCATCCCC | ATTACCTGAG | ACTACAGGCG | 16500 |
| CGCACCACCA | CACCGGCTGA | CTTTTATGTT | GTTTCTCATG | TTTTCCGTAG | GTAGGTATGT | 16560 |
| GTGTGTGTGT | GTGTGTGTGT | GTGTGTGTGT | GTGTGTGTGT | GTGTGTGTGT | GTGTGTATCT | 16620 |
| ATGTATGTAC | GTATGTATGT | ATGTATGTGA | GTGAGATGGG | TTTTCGGGGT | CTATCATGTT | 16680 |
| GCCACGCTG | GTCTCGAACT | CCTGTCTCTA | AGCAATCCGC | CTGCCTGCCT | CGGCCGCCCA | 16740 |
| CACTGCTGCT | ATTACAGGCG | TGAGACGCTG | CGCCTGGCTC | CTTCTACATT | TGCCCTGCCTG | 16800 |
| CCTGCCTGCC | TGCCTGCCTA | TCAATCGTCT | TCTTTTTTAGT | ACGGATGTCG | TCTCGCTTTA | 16860 |
| TTGTCCATGC | TCTGGGCACA | CGTGGTCTCT | TTTCAAACCT | CTATGATTAT | TATTATTGTA | 16920 |
| GGCGTCATCT | CACGTGTCGA | GGTGATCTCG | AACTTTTAGG | CTCCAGAGAT | CCTCCCGCAT | 16980 |
| CGGCCTCCCC | GAGTGCTGTG | ATGACACGCG | TGGGCACGGT | ACGCTCTGGT | CGTGTGTTGTC | 17040 |
| GTGGGTCCGT | TCTTTCCGTT | TTTAATACGG | GGACTGCGAA | CGAAGAAAAAT | TTTCAGACGC | 17100 |
| ATCTCACCAG | TCCGCCTTTT | CGTTCCTTCT | TTTTATTCTC | TTTAGACGGA | GTTTCACTCT | 17160 |
| TGTCGCCCCAG | GGTGGAGTAC | GATGGCGGCT | CTCGGCTCAC | CGCACCCCTCC | GCCTCCGAGG | 17220 |
| TTCAAGTGAT | TCTCCTGCCT | CAGCCTTCCC | GAGTAGCTGG | AATGACAGAG | ATGAGCCATC | 17280 |
| GTGCCCGGCT | AATTTTTCTA | TTTTTAGTAC | AGATGGGGTT | TCTCCATCTT | GGTCAGGCTG | 17340 |
| GTCTTCAACT | TCCGACCGTT | GGAGAATCTT | AACTTTCTTG | GTGGTGTTTG | TTTTCTTTTT | 17400 |
| TCTTTTTTTT | TCTTTTCTTT | CTTTTCTTTC | TCCTCCCCCC | CCCACCCCTCC | TTGTCGCTGT | 17460 |
| CCTCCTCCTC | CTCCTCCTCC | TCCTCCTCCT | CCTCCTCCTC | CTCCTCCTCC | TCTTTCATTT | 17520 |
| CTTTCAGCTG | GGCTCTCCTA | CTTGTGTTGC | TCTGTTGCTC | ACGCTGGTCT | CAAACCTCTG | 17580 |
| GCCTTGACTC | TTCTCCCGTC | ACATCCGCCG | TCTGTTGTTT | GAAATGAGCA | TCTCTCGTAA | 17640 |
| AATGGAAAG | ATGAAAGAAA | TAAACACGAA | GACGGAAAGC | ACGGTGTGAA | CGTTTCTCTT | 17700 |
| GCCGTCTCCC | GGGGGTGTAC | TTGGACCCGG | AAACACGGAG | GGAGCTTGGC | TGAGTGGGTT | 17760 |
| TTCCGTTGCCG | AAACCTCCCG | AGGGCCTCCT | TCCCTCTCCC | CCTTGTCCCC | GCTTCTCCGC | 17820 |
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| ACCTGCCACC | TTCCAGGGAG | CTCTGAGGCG | GATGCCAGCC | CCACCCCTCC | GTACGTTCCC | 18000 |
| GCTACCCCTCC | CCCGGCTGGC | CTTTGCCGGG | CGACCCACAG | GGAAACCGCT | TGATGCTGCT | 18060 |
| TCGGATCCTC | CGGCGAAGAC | TTCCACCGGA | TGCCCCGGGT | GGGCCGGTTG | GGATCAGACT | 18120 |
| GGACCACCCC | GGACCGTGCT | GTTCTTGGGG | GTGGGTTGAC | GTACAGGGTG | GACTGGCAGC | 18180 |
| CCCAGCATTG | TAAAGGGTGC | GTGGGTATGG | AAATGTCACC | TAGGATGCCC | TCCTTCTCCT | 18240 |
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| CCTTTCTCCA | GCACACAGAT | GAGACGCACG | AGAGGGAGAA | ACAGCTCAAT | AGATACCGCT | 18360 |
| GACCTTCATT | TGTGGAATCC | TCAGTCATCG | ACACACAAGA | CAGGTGACTA | GGCAGGGACA | 18420 |
| CAGATCAAAC | ACTATTTCCG | GGTCCTCTGT | GTGGGATTGG | TCTCTCTCTC | TCTCTCTCTC | 18480 |
| TCTCTCTCTC | TCTCTCTCTC | TCTCGCACGC | GCACGCGCGC | ACACACACAC | ACAATTTCCA | 18540 |
| TATCTAGTTT | ACAGAGCACA | CTCACTTCCC | CTTTTACACG | TACGCAAGGCT | GAGTAAAACG | 18600 |
| CGCCCCACCC | TCCACCCGTT | GGCTGACGAA | ACCCCTTCTC | TACAATTGAT | GAAAAAGATG | 18660 |
| ATCTGGGCCG | GGCACGCTAG | CTCACGCCTG | TCACTCCGGC | ACTTTGGGAG | GCCGAGGCGG | 18720 |
| GTGGATCGCT | TGGGGCCGGG | AGTTCGAGAC | CAGGCTGGCC | GACGTGGCGA | AACCCCGTCT | 18780 |
| CTCTGAAAAA | TAGAACGATT | AGCCGGGCCCT | GGTGGCGTGG | GCTTGAATC | ACGACCGCTC | 18840 |
| GGGAGACTGG | GGCGGGCGAC | TTGTTCCAAC | CGGGGCGGCC | GAGGCGCGCA | TGAGCTGAGA | 18900 |
| TCGTGCCGTG | GCGATGCGGC | CTGGATGACG | GAGCGAGACC | CCGTCTCGAG | AGAATCATGA | 18960 |
| TGTTATTATA | AGATGAGTTG | TGCGCGGTGA | TGGCCGCTTG | TAGTCGCGGC | TACTCGGGAG | 19020 |

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| GCTGAGACGA | GGAGAAGATC | ACTTGAGGCC | CCACAGGTCG | AGGCTTCGGT | CGGCCGTGAC | 19080 |
| CCACTGTATC | CTGGGCAGTC | ACCGGTCAAG | GAGATATGCC | CCTTCCCCGT | TTGCTTTTCT | 19140 |
| TTTCTTCCCT | TCTCTTTTCT | TCTTTTGTCT | TCTCTTTTCT | TTCTTTTCTT | CTTCTTTTCT | 19200 |
| TTCTTTCTTT | CTTTCTTTCT | TTTTCTTTTT | CTCTCTTCCC | CTCTTTCTTT | CCTGCCTTCC | 19260 |
| TGCCTTTCTT | CTTTTCTTCT | TTCCTCCCTT | CCTCCCTTCC | TTCTTTCTCT | CCGCTCAGC | 19320 |
| CTCCCAAAGT | GCTGGGATGA | CTGGCGGGAG | GCACCATGCC | TGCTTGGCCC | AAAGAGACCC | 19380 |
| TCTTGGAAAG | TGAGACGCAG | AGAGCGCCTT | CCAGTGATCT | CATTGACTGA | TTAGAGACG | 19440 |
| GCATCTCGCT | CCGTCACCCC | GGCAGTGGTG | CCGTCGTAAC | TCACTCCCTG | CAGCGTGGAC | 19500 |
| GCTCCTGGAC | TGCAGCGATC | CTTCCACCTC | AGCCTCCAGA | GTACAGAGCC | TGGGACCGCG | 19560 |
| GGCACGCGCC | ACTGTGCCCA | CACCGTTTTT | AATTGTTTTT | TTTTCCCCCG | AGACAGAGTT | 19620 |
| TCACTCTCGT | GGCCTAGACT | GCAGTGCCTG | GGCGCGATCT | TGGCTCACCG | CAACCTCTGC | 19680 |
| TTCCCGGTTT | CAAGCGATTG | TCCGTGCATC | GCCTCTGAG | TAGCCGGGAT | TGCGGGCATG | 19740 |
| CGCTGCCACG | TCTGGCTGAT | TTCGTATTTT | TAGTGAGAGC | GGGGCTTCTC | CATGTCGATC | 19800 |
| GGGCTGGTTT | CGAACTCCCG | ACCTCAGGTG | ATCCGCCCTC | CCCGGCCTCC | GGAAGTGCTG | 19860 |
| GGATGACAGG | CGTGAGCCAC | CGCGCCCGGC | CTTCATTTTT | AAATGTTTTT | CCACAGACGG | 19920 |
| GGTCTCATCA | TTTCTTTGCA | ACCCTCCTGC | CCGGCGTCTC | AAAGTGCTGG | CGTGACGGGC | 19980 |
| GTGAGCCACT | GCGCTGGGAC | TCCGGGGAAT | GACTCACGAC | CACCATCGCT | CTACTGATCC | 20040 |
| TTTCTTTCTT | TCTTTCTTTC | TTTCTTTCTT | TCTTTCTTTC | TTTCTTTCTT | TCTTTCTTGA | 20100 |
| TGAATTATCT | TATGATTTAT | TTGTGTACTT | ATTTTCAGAC | GGAGTCTCGC | TCTGGGCGGG | 20160 |
| GCGAGGCGAG | GCGAGGCACA | GCGCATCGCT | TTGGAAGCCG | CGGCAACGCC | TTTCAAAGCC | 20220 |
| CCATTTCGTAT | GCACAGAGCC | TTATTCCCTT | CCTGAGTTTG | GAGCTGATGC | CTTCCGTAGC | 20280 |
| CTTGGGCTTC | TCTCCATTCT | GAAGCTTGAC | AGGCGCAGGG | CCACCCAGAG | GCTGGCTGCG | 20340 |
| GCTGAGGATT | AGGGGGTGTG | TTGGGGCTGA | AAACTGGGTC | CCCTATTTTT | GATACCTCAG | 20400 |
| CCGACACATC | CCCCGACCGC | CATCGCTTGC | TGCGCCTCTG | AGATCCCCCG | CCTCCACCGC | 20460 |
| CTTGCAGGCT | CACCTCTTAC | TTTCATTTCT | TCTTTCTTTC | CGTTTGAGGA | GGGGGTGCGG | 20520 |
| GAATGAGGGT | GTGTGTGGGG | AGGGGGTGCG | GGGTGGGGAC | GGAGGGGAGC | GTCTTAAGGG | 20580 |
| TCGATTTAGT | GTCATGCCCT | TTTACCACCC | ACCACCACCA | CCGAAGATGA | CAGCAAGGAT | 20640 |
| CGGCTAAATA | CCGCGTGTTC | TCATCTAGAA | GTGGGAACCT | ACAGATGACA | GTCTTGCAT | 20700 |
| GGGCGAAGC | AGGGGGACCG | GGGACGCGGA | AGTCTGCTTG | AGGGAGGAGG | GGTGGAAGGA | 20760 |
| GAGACAGCTT | CAGGAAGAAA | ACAAAACACG | AATACTGTCT | GACACAGCAC | TGACTACCCG | 20820 |
| GGTGATGAAA | TCATCTGCAC | ACTGAACACC | CCCGTCACAA | GTTTACCTAT | GTCACAATCT | 20880 |
| TGCACATGTA | TCGCTTGAAC | GACAAATAAA | AGTTAGGGGG | GAGAAGAGAG | GAGAGAGAGA | 20940 |
| GAGAGAGAGA | GACAGAGAGA | GACAGAGAGA | GAGAGAGAGG | AGGGAGAGAG | GAAAAACGAA | 21000 |
| CACCACCTCC | TTGACCTGAG | TCAGGGGGTT | TCTGGCCTTT | TGGGAGAACG | TTCAGCGACA | 21060 |
| ATGCAGTATT | TGGGCCCGTT | CTTTTTTTTT | CTTCTCTTTT | TCTTTCTTTT | TTTCTGGACT | 21120 |
| GAGTCTCTCT | CGCTCTGTCA | CCCAGGCTGC | GGTCGCGGTG | GCGCTCTCTC | GGCTCACTGA | 21180 |
| AACCTCTGCT | TCCCGGGTTC | CAGTGATTCT | TCTTCGGTAG | CTGGGATTAC | AGGCGCACAC | 21240 |
| CATGACGGCG | GGCTCATATT | CCTATTTTCA | GTAGAGACGG | GGTTTCTCCA | CGTTGGCCAC | 21300 |
| GCTGGTCTCG | AACTCCTGAC | CTCAAATGAT | CCGCCTTCTT | GGGCCCTCCA | AAGTGCTGGA | 21360 |
| AACGACAGGC | CTGAGCCGCG | GGGATTTTCAG | CCTTTAAAG | CGCGGCCCTG | CCACCTTTCG | 21420 |
| CTGTGGCCCT | TACGCTCAGA | ATGACGTGTC | CTCTCTGCCG | TAGGTTGACT | CCTTGAGTCC | 21480 |
| CCTAGGCCAT | TGCACTGTAG | CCTGGGCAGC | AAGAGCCAAA | CTCCGNCCCC | CCACCTCCTC | 21540 |
| GCGCACATAA | TAACTAACTA | ACAACTAAAC | TAACTAACTA | AACTAACTAA | CTAACTAAAA | 21600 |
| TCTCTACACG | TCACCCATAA | GTGTGTGTTT | CCGTGAGAGT | GATTTCTAAG | AAATGGTACT | 21660 |
| GTACACTGAA | CGCAGTGGCT | CACGTCTGTC | ATCCCAGAGT | CAGGAGTTCT | AGACCAGCCC | 21720 |
| GGCCAACGTG | GTGAAACCCC | GTCTCTACTG | AAAATACGAA | ATGGAGTCAG | GCGCCGTGGG | 21780 |
| GCAGGCACCT | GTAACCCACG | CTACTCGGGA | GGCTGGGGTG | GAAGAATTGC | TTGAACCTGG | 21840 |
| CAGGCGGAGG | CTGCAGTGAC | CCAAGATCGC | ACCACTGCAC | TACAGCCTGG | GCGACAGAGT | 21900 |
| GAGACCCGGT | CTCCAGATAA | ATACGTACAT | AAATAAATAC | ACACATACAT | ACATACATAC | 21960 |
| ATACATACAT | ACATACATAC | ATCCATGCAT | ACAGATATAC | AAGAAAGAAA | AAAAGAAAAG | 22020 |
| AAAAGAAAGA | GAAAATGAAA | GAAAAGGCAC | TGTATTGCTA | CTGGGCTAGG | GCTTCTCTCT | 22080 |
| TGTCTGTTTC | TCTCTGTTTC | TCTCTGTCTT | TCTCTCTGTG | TCTCTTTCTC | TGTCTGTCTG | 22140 |
| TCTCTTTCTT | TCTCTCTGTC | TCTGTCTCTG | TCTTTGTCTC | TCTCTCTCCC | TCTCTGCCTG | 22200 |
| TCTCACTGTG | TCTGTCTTCT | GTCTTACTCT | CTTTCTCTCC | CCGTCTGTCT | CTCTCTCTCT | 22260 |
| CTCTCCCTCC | CTGTTTGTTC | CTCTCTCTCC | CTCCCTGTCT | GTTTCTCTCT | CTCTCTTTCT | 22320 |
| GTCTGTTTCT | GTCTCTCTCT | GTCTGTCTAT | GTCTTTCTCT | GTCTGTCTCT | TTCTCTGTCT | 22380 |
| GTCTGCCTCT | CTCTTTCTTT | TTCTGTGTCT | CTCTGTCTGG | CTCTCTCTCT | CTGTCTGTCT | 22440 |
| GTCTGTCTCT | TCTCTCTCTT | CTCTGTCTCT | ATCTCTGTCT | TTACTCTCTT | TCTCTGCCTG | 22500 |
| TCTGTCTGTC | TCTCCCTCCC | TTTCTGTTTC | TCTCTCTCTC | TCTCTCTCTC | TCCCCCTCTC | 22560 |
| CCTGTCTGTT | TCTCTCCGTC | TCTCTCTCTT | TCTGTCTGTT | TCTCACTGTC | TCTCTCTGTC | 22620 |
| CATCTCTCTC | TCTCTCTGTC | TGTCTCTTTC | GTTCTCTCTG | TCTGTCTGTC | TCTCTCTCTC | 22680 |
| TCTCTCTCTC | TCTCTCTCTC | TCCCTGTCTG | TCTGTTTCTG | TCTATCTCTC | GCTGTCCATC | 22740 |
| TCTGTCTTTC | TATGTCTGTC | TCTTCTCTCT | TCAGTCTGTC | AGACACCCCC | GTGCGGGGTA | 22800 |
| GGGCCCTGCC | CCTTCCACGA | AAGTGAGAAG | CGCGTGCTTC | GGTGCTTAGA | GAGGCCGAGA | 22860 |
| GGAATCTAGA | CAGGCGGGCC | TTGCTGGGCT | TCCCCACTCG | GTGTATGATT | TCGGGAGGTC | 22920 |

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| GAGGCCGGGT | CCCCGCTTGG | ATGCGAGGGG | CATTTTCAGA | CTTTTCTCTC | GGTCACGTGT | 22980 |
| GGCGTCCGTA | CTTCTCCTAT | TTCCCCGATA | AGCTCCTCGA | CTTCAACATA | AACGGCGTCC | 23040 |
| TAAGGGTCGA | TTTAGTGTCA | TGCCTCTTTC | ACCGCCACCA | CCGAAGATGA | AAGCAAAGAT | 23100 |
| CGGCTAAATA | CCGCGTGTTC | TCATCTAGAA | GTGGGAACTT | ACAGATGACA | GTTCTTGCAT | 23160 |
| GGGCAGAACG | AGGGGGACCG | GGNACGCGGA | AGCCTGCTTG | AGGGRGGAGG | GGYGGAAGGA | 23220 |
| GAGACAGCTT | CAGGAAGAAA | ACAAAACACG | AATACTGTCT | GACACAGCAC | TGACTACCCG | 23280 |
| GGTGATGAAA | TCATCTGCAC | ACTGAACACC | CCCGTCACAA | GTTTACCTAT | GTCACAGTCT | 23340 |
| TGCTCATGTA | TGCTTGAACG | ACAAATAAAA | GTTCGGGGGG | GAGAAGAGAG | GAGAGAGAGA | 23400 |
| GAGAGACGGG | GAGAGAGGGG | GGAGAGGGGG | GGGGAGAGAG | AGAGAGAGAG | AGAGAGAGAG | 23460 |
| AGAGAGAGAG | AGAAAGAGAA | GTAAAACCAA | CCACCACCTC | CTTGACCTGA | GTCAGGGGGT | 23520 |
| TTCTGGCCTT | TTGGGAGAAC | GTTCAGCGAC | AATGCAGTAT | TTGGGCCCCG | TCTTTTTCCT | 23580 |
| TTCTTCTTCT | TTTCTTTCTT | TTTTTTTGGG | CTGAGTCTCT | CTCGCTCTGT | CACCCAGGCT | 23640 |
| GCGGTGCGGT | GGCGCTCTCT | CGGCTCACTG | AAACCTCTGC | TTCCCGGGTT | CCAGTGATTC | 23700 |
| TTCTTCGGTA | GCTGGGATTA | CAGGTGCGCA | CCATGACGGC | CGGCTCATCG | TTCTATTTTT | 23760 |
| AGTAGAGACG | GGGTTTCTCC | ACGTTGGCCA | CGCTGGTCTC | GAACCTCCTGA | CCACAAATGA | 23820 |
| TCCACCTTCC | TGGGCCTCCC | AAAGTGTCTG | AAACGACAGG | CCTGAGCCCG | CGGGATTCTA | 23880 |
| GCCTTTAAAA | GCGCGCGGCC | CTGCCACCTT | TGCTGCGGGC | CCTTACGCTC | AGAATGACGT | 23940 |
| GTCTCTCTCT | CCATAGGTTG | ACTCCTTGAG | TCCCCTAGGC | CATTGCACTG | TAGCCTGGGC | 24000 |
| AGCAAGAGCC | AAACTCCGTC | CCCCCACCTC | CCCGCGCACA | TAATAACTAA | CTAACTAACT | 24060 |
| AACTAACTAA | AATCTCTACA | CGTCACCCAT | AAGTGTGTGT | TCCCGTGAGG | AGTGATTCTT | 24120 |
| AAGAAATGGT | ACTGTACACT | GAACGCAGGC | TTCACGTCTG | TCATCCCGAG | GTCAGGAGTT | 24180 |
| CGAGACCAGC | CCGGCCACAG | TGGTGAAACC | CCCGTCTCTA | CTGAAAATAC | GAAATGGAGT | 24240 |
| CAGGCGCCGT | GGGGCAGGCA | CCTGTAACCC | CAGCTACTCG | GGAGGCTGGG | GTGGAAGAAT | 24300 |
| TGCTTGAACC | TGGCAGGCGG | AGGCTGCAGT | GACCCAAGAT | CGCACCCTG | CACTACAGCC | 24360 |
| TGGGCGACAG | AGTGAGACCC | GGTCTCCAGA | TAAATACGTA | CATAAATAAA | TACACACATA | 24420 |
| CATACATACA | TACATACAAC | ATACATACAT | ACAGATATAC | AAGAAAGAAA | AAAAGAAAAG | 24480 |
| AAAAGAAAGA | GAAAATGAAA | GAAAAGGCAC | TGTATTGCTA | CTGGGCTAGG | GCCTTCTCTC | 24540 |
| TGTCTGTTTC | TCTCTGTTCG | TCTCTGTCTT | TCTCTCTGTG | TCTCTTTCTC | TGTCTGTCTG | 24600 |
| TCTGTCTGTC | TGTCTGTCTC | TTTCTTTCTT | TCTGTCTCTG | TCTTTGTCCC | TCTCTCTCCC | 24660 |
| TCTCTGCCCT | TCTCTCACTG | GTCTGTCTTC | TATCTTACTC | TCTTTCTCTC | CCCGTCTGTC | 24720 |
| TCTCTCTCAC | TCCCTCCCTG | TCTGTTTCTC | TCTCTCTCTC | TTTCTGTCTG | TTTCTGTCTC | 24780 |
| TCTCTGTCTG | CCTCTCTCTT | TCTCTATCTG | TCTCTTTCTC | TGTCTGTCTG | CCCTCTCTCT | 24840 |
| TCTTTTTCTG | TGTCTCTCTG | TCTGTCTCTC | TCTCTCTCTG | TGCCTATCTT | CTGTCTTACT | 24900 |
| CTCTTTCTCT | GCCTGTCTGT | CTGTCTCTCT | CTGTCTCTCC | CTCCCTTTCT | GCTTCTCTCT | 24960 |
| TCTCTCTCTC | CTCTNNNCCC | TCCCTGTCTG | TTTCTCTCTG | TCTCCCTCTC | TTTCTGTCTG | 25020 |
| TTTCTCACTG | TCTCTCTCTG | TCTGTCTGTT | TCATTCTCTC | TGTCTCTGTC | TCTGTCTCTC | 25080 |
| TCTCTCTCTG | TCTCTCCCTC | TCTGTGTGTA | TCTTTTGTCT | TACTCTCCTT | CTCTGCCTGT | 25140 |
| CCGTCTGTCT | GTCTGTCTCT | CTCTCTCCCT | GTCCCTCTCT | CTTTCTGTCT | GTTTCTCTCT | 25200 |
| CTCTCTCTCT | CTCTCTCTCT | CTGTCTCTGT | CTTTCTCTGT | CTGTCCCTTT | CTCTGTCTGT | 25260 |
| CTGCCCTCTC | CTTTCTCTTT | CTGTGTCTCT | CTGTCTCTCT | CTCTGTGCCT | ATCTTCTGTC | 25320 |
| TTACTCTCTT | TCTCTGCCTG | TCTATCTGTC | TGTCTCTCTC | TGTCTCTCTC | CCTGCCTTTC | 25380 |
| TGTTTTCTCT | TCTCTCCCTC | TCTCGCTCTC | TCTGTCTTTT | TCTCTTTTCT | TCTGTTTCTC | 25440 |
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| GTCTGTCTCT | GTCTGTCTCT | GTCTCTCTCT | CTCTCTCTCT | CTCCTTGTCT | CTCTCACTGT | 25560 |
| GTCTGTCTTC | TGTCTTACTC | TCCTTCTCTG | CCTGTCCATC | TGTCTGTCTG | TCTCTCTCTC | 25620 |
| TCTCTCCCTA | CCTTCTGTGT | TCTCTCTCGC | TAGCTCTCTC | TCTCTCTGCC | TGTTTCTCTC | 25680 |
| TTTCTCTCTC | TGTCTTTTCT | TGTCTGTCTC | TTTCTCTGTC | TGTCTGTCTC | TTTCTCTCTG | 25740 |
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| ATCTTCTGTC | TTACTCTGTT | TCCTTGCCTG | CCTGCCTGTC | TGTGTGTCTG | TCTCTCTCTC | 26040 |
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| CCCTCTCTCT | CCCTCCCTTT | CTGTTTCTCT | CTCTCTCTCT | TTCTGTCTGT | TTCTCTCTTT | 26340 |
| CTCTCTCTGT | CTGTCTCTTT | CTGTCTCTGT | CTGTCTCTCT | CTTTCTTTT | CTCTGTCTCT | 26400 |
| CTGTCTCTCT | CTGTGTCTGT | CTCTCTGTCT | GTGCCTATCT | TCTGTCTTAC | TCTCTTTCTC | 26460 |
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| TCTCTTTCTT | TTTCTCTGTC | TCTCTGTCTC | TCTCTGTGTC | TGTCTCTCTT | TCTGTGCTTA | 26640 |
| TCTTCTGTCT | TACTCTCTTT | CTCTGGCTGT | CTGCCTGTCT | CTCTCTCTCT | GCCTGTCTCC | 26700 |
| GTCCCTCCCT | CCCTGTCTGT | CTGTTTCTCT | CTCTGTCTCT | GTCTCTCTGT | CCATCTCTGT | 26760 |
| CTGTCTCTTT | CTCTTTCTCT | CTCTCTGTCT | CTGTCTCTCT | CTCTCTCTGC | CTGTCTCTCT | 26820 |

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| CACTGTGTCT | GTCTTCTGTC | TTACTCTCTT | TCTCTTGCC | GCCTCTCTGT | CTGTCTGTCT | 26880 |
| CTCTCCCTCC | ATGTCTCTCT | CTCTCTCTCA | CTCACTCTCT | CTCCGTCTCT | CTCTCTTTCT | 26940 |
| GTCTGTTTCT | CTCTCTGTCT | GTCTCTCTCC | CTCCATGTCT | CTCTCTCTCT | CTCTCACTCA | 27000 |
| CTCTCTCTCC | GTCTCTCTCT | CTCTTTCTGT | CTGTTTCTCT | CTCTGTCTGT | CTCTCTCCCT | 27060 |
| CCATGTCTCT | CTCTCTCCCT | CTCACTCACT | CTCTCTCCGT | CTCTCTCTCT | CTTTCTGTCT | 27120 |
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| CTCTGTCTCT | CTCTCTTTCT | CTTTCTGTCT | GTTTCTCTCT | ATCTCTCGCT | GTCCATCTCT | 27300 |
| GTCTTTCTAT | GTCTGTCTCT | TTCTCTGTCA | GTCTGTGAGA | CACACCCGTG | CCGGTAGGGC | 27360 |
| CCTGCCCTTC | CACGAGAGTG | AGAAGCGCGT | GCTTCGGTGC | TTAGAGAGGC | CGAGAGGAAT | 27420 |
| CTAGACAGGC | GGGCCTTGCT | GGGCTTCCCC | ACTCGGTGTA | CGATTTCGGG | AGGTCGAGGC | 27480 |
| CGGGTCCCGG | CTTGGATGCG | AGGGGCATTT | TCAGACTTTT | CTCTCGGTCA | CGTGTGGCGT | 27540 |
| CCGTACTTCT | CCTATTTCCT | CGATAAGTCT | CCTCGACTTC | AACATAAACT | GTTAAGGCCG | 27600 |
| GACGCCAACA | CGGCAGAAC | CCGTCTCTAC | TAAAAATACA | AAGCTGAGTC | GGGAGCGGTG | 27660 |
| GGGCAGGCC | TGTAATGCCA | GCTCCTCGGG | AGGCTGAGGC | GGGAGAATCG | CTTGAACCAG | 27720 |
| GGAAGCGGAG | GCTGCAGGGA | GCCGAGATCG | CGCCACTGCA | CTACGGCCCA | GGCTGTAGAG | 27780 |
| TGAGTGAGAC | TCGGTCTCTA | AATAAATACG | GAAATTAAAT | AATTCAATTA | TTCTTTTCCC | 27840 |
| TGCTGACGGA | CATTTGCAGG | CAGGCATCGG | TTGTCTTCGG | GCATCACCTA | GCGGCCACTG | 27900 |
| TTATTGAAAG | TCGACGTTGA | CACGGAGGGA | GGTCTCGCCG | ACTTCACCGA | GCCTGGGGCA | 27960 |
| ACGGGTTTCT | CTCTCTCCCT | TCTGGAGGCC | CCTCCCTCTC | TCCCTCGTTG | CCTAGGGAAC | 28020 |
| CTCGCTTAGG | GAACCTCCGC | CCTGGGGGCC | CTATTGTTCT | TTGATCGGCG | CTTTACTTTT | 28080 |
| CTTTGTGTTT | TGGCGCCTAG | ACTCTTCTAC | TTGGGCTTTG | GGAAGGGTCA | GTTTAATTTT | 28140 |
| CAAGTTGCC | CCCGGCTCCC | CCCACTACCC | ACGTCCCTTC | ACCTTAATTT | AGTGAGNCGG | 28200 |
| TTAGGTGGGT | TTCCCCCAAA | CCGCCCCCCC | CCCCCGCCT | CCCAACACCC | TGCTTGGA | 28260 |
| CCTTCAGAG | CCACCCCGGT | GTGCCCTCCG | CTTCTCTCCC | CTTCCCCAC | CCCTTGCCGG | 28320 |
| CGATCTCAT | CTTGCCAGGC | TGACATTTGC | ATCGGTGGGC | GTCAGGCCTC | ACTCGGGGGC | 28380 |
| CACCGTTTTT | GAAGATGGGG | GCGGCACGGT | CCCACTTCCC | CGGAGGCAGC | TTGGGCCGAT | 28440 |
| GGCATAGCCC | CTTGACCCGC | GTGGGCAAGC | GGGCGGGTCT | GCAGTTGTGA | GGCTTTTCCC | 28500 |
| CCCCTGCTT | CCCCTCAGG | CCTCCCTCCC | TAGGAAAGCT | TCACCCTGGC | TGGGTCTCGG | 28560 |
| TACCTTTTA | TCACGATGTT | TTAGTTTCTC | CGCCCTCCGG | CCAGCAGAGT | TTCAACAATG | 28620 |
| GAAGGGCGCC | ACGGCTCTAG | TCTGGGCCTT | CTCAGTACTT | GCCCAAAATA | GAAACGCTTT | 28680 |
| CTGAAACTA | ATAACTTTNC | TCACTTAAGA | TTTCCAGGGA | CGGCGCCTTG | GCCCCTGTTT | 28740 |
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| CACGTAGCT | GCCGTTTTTT | CCTGTTGTGA | ACTAGCGCTT | TTGTGACTCT | CTCAACGCTG | 28920 |
| CAGTGAGAGC | CGGTTGATGT | TTACNATCCT | TCATCATGAC | ATCTTATTTT | CTAGAAATCC | 28980 |
| GTAGGCGAAT | GCTGCTGCTG | CTCTTGTTGC | TGTTGTTGTT | GTTGTTGTTG | TCGTCTGTTG | 29040 |
| TGTTGTCGTT | GTCGTTGTTG | TTGTCGTTGT | CGTTGTTTTT | AAAGTATACC | CCGGCCACCG | 29100 |
| TTTATGGGAT | CAAAAGCAT | ATAAAATATG | TGTGATTATT | TCTTGAGCAC | GCCCTTCCCT | 29160 |
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| CTCTCTCTCT | CTGTGTCTCT | CTCTCTCTGC | CTGTCTGTTT | CTCTCTCTCT | GCCTCTCTCT | 29280 |
| CTCTCTCTCT | CTCTGCTGTT | CTCTCTCACT | GTGTCTGTCT | TCTGTCTTAC | TCCCTTTCTC | 29340 |
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| CTCTCTCTCT | CTCCCTGTCT | GTCTGTCTCT | CTCTCTCTCT | CCCCCTGTCT | GTTTCTCTCT | 29760 |
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| CTCTCTGTGT | GTCTGTCTTC | TGTCTTACTG | TCTTTCTCTG | CCTGTCTGTC | TGTCTGTCTC | 29880 |
| TCTCTGTCTG | TCTCTCTCTC | TCTCTCCCCC | TGTCTGCTGT | TTCTCTGTCT | CTGTCTGTGT | 29940 |
| CTCTCTTTCT | GTCTGTTTCT | CTCTGTCTGT | CTTCTCTCTC | CTGTCTCTTT | CTCTCTGTCT | 30000 |
| CTCTGTCTGT | CTCTGTCTCT | CTCTCTGTCT | CTCTCTCTCT | GTGGGGGTGT | GTGTGTGTGT | 30060 |
| GTGTATGTGT | GTGTGTGTGT | GTGTGTGTGT | CTGCCTTCTG | TCTTACTCTC | TTTCTCTGCC | 30120 |
| TGTCTGTCTG | CCTGTCTGTT | TGTCTCTCTC | TCTCTGCCTG | TCTCTCTCCC | TTCTGTCTG | 30180 |
| TTTCTCTCTC | TTTCTGTTTC | TCTCTGTCTC | TGTCCATCTC | TGTCTTTCTC | CGTCTGTCTC | 30240 |
| TTTATCTGTC | TCTCTCCGTC | TGTCTCTTTA | TCTGTCTCTC | TCTCTCTTTT | TGTCTTTCTC | 30300 |
| TCTCTGTGTA | TCGTTGTCTC | TCTCTGTCTG | TCTCTGTCTC | TGTCTCTCTG | TCTCTCTCTC | 30360 |
| TCTCTCTCTC | TCTCTGTCTG | TCTGTCCGTC | TGTCTGTCTC | GGTCTCTGCG | TCTCGCTATC | 30420 |
| TCCCGCCCTC | TCTTTTTTTG | CAAAAGAAGC | TCAAGTACAT | CTAATCTAAT | CCCTTACCAA | 30480 |
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| ACTGGCGAGT | TGATTTCTGG | ACTTGGATAC | CTCATAGAAA | CTACATATGA | ATAAAGATCC | 30600 |
| AATCCTAAAA | TCTGGGGTGG | CTTCTCCCTC | GACTGTCTCG | AAAAATCGTA | CCTCTGTTCC | 30660 |
| CCTAGGATGC | CGGAAGAGTT | TTCTCAATGT | GCATCTGCCC | GTGTCTTAAG | TGATCTGTGA | 30720 |

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| ACTACCCACG | GCCCCCTGTG | GAACCACTGG | CTCTTTGAAA | AAAATCCCAG | AAGTGGTTTT | 30840 |
| GGCTTTTTTG | CTAGGAGGCC | TAAGCCTGCT | GAGAACTTTC | CTGCCCAGGA | TCCTCGGGAC | 30900 |
| CATGCTTGCT | AGCGCTGGAT | GAGTCTCTGG | AAGGACGCAC | GGGACTCCGC | AAAGCTGACC | 30960 |
| TGTCCCACCG | AGGTCAAATG | GATACCTCTG | CATTGGCCCC | AGGCCTCCGA | AGTACATCAC | 31020 |
| CGTCACCAAC | CGTCACCGTC | AGCATCCTTG | TGAGCCTGCC | CAAGGCCCCG | CCTCCGGGGA | 31080 |
| GACTCTTGCG | AGCCCCGGCT | TCGTGGGCTA | AAGTCCAAAG | GGATGGTGAC | TTCCACCCAC | 31140 |
| AAGGTCCCAC | TGAACGGCGA | AGATGTGGAG | CGTAGGTTCAG | AGAGGGGACC | AGGAGGGGAG | 31200 |
| ACGTCCCCGAC | AGGCGACGAG | TTCCCAAGGC | TCTGGCCACC | CCACCCACGC | CCCACGCCCC | 31260 |
| ACGTCCCCGGG | CACCCGCGGG | ACACCGCCGC | TTTATCCCTT | CCTCTGTCCA | CAGCCGGCCC | 31320 |
| CACCCACACA | CGCAACCCAC | GCACACACGC | TGGAGGTTTC | AAAACCACAC | GGTGTGACTA | 31380 |
| GAGCCTGACG | GAGCGAGAGC | GCATTTTCAC | AGGTGGGAGG | GGTGGGGGTG | GGGTGGGTTG | 31440 |
| GGGGTTGTGG | GGTCTGTGGC | GAGCCCGATT | CTCCCTCTTG | GGTGGCTACA | GGCTAGAAAT | 31500 |
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| TCTCAGCGCC | ACCATGGCCG | GCTCATTTTT | TTTTTTTTTT | TTTTTGGTAG | ACACGGGGTT | 31860 |
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| AAAGTTGCTC | AGTATTTAGA | AGCTACCTAA | ATACGTCAGC | ATTTACACTC | TTCTAGTAA | 32160 |
| AAGCTGGCCG | ATCTGAATAA | TCCTCCTTTA | AACAAACACA | ATTTTGTATA | GGGTAAAGAT | 32220 |
| TTTTTTAAGA | ATGCCACTCC | TGCAAAATAG | CTGAACAGAC | GATACACATT | TAAAAAATA | 32280 |
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CCTCGGGAAG AGCTTCTCGA CTCACGTTTT CGCTTTCGCG GTCCACGGGC CGCCCTGCCA 42060
GCCGATCTG TCTCGCTGAC GTCCGCGGCG GTTGTCGGGC TCCATCTGGC GGCCGCTTTG 42120
AGATCGTGCT CTCGGCTTCC GGAGCTGCGG TGGCAGCTGC CGAGGGAGGG GACCGTCCCC 42180
GCTGTGAGCT AGGCAGAGCT CCGGAAAGCT CGCGGTCTGT AGCCCGGCTG GCCCGGTGGC 42240
GCCAGAGCTG TGGCCGGTCC CTTGTGAGTC ACAGCTCTGG CGTGAGGTT TATGTGGGG 42300
AGAGGCTGTC GCTGCGCTTC TGGGCCGCG GCGGGCGTGG GGCTGCCCCG GCCGGTCGAC 42360
CAGCGCGCCG TAGCTCCCGA GGCCCGAGCC GCGACCCGGC GGACCCGCCG CGCGTGCGCG 42420

```

```

AGGCTGGGGA CGCCCTTCCC GGCCCGGTCTG CGGTCCGCTC ATCCTGGCCG TCTGAGGCGG 42480
CGGCCGAATT CGTTTCCGAG ATCCCCGTGG GGAGCCGGGG ACCGTCCCCG CCCCCTCCCC 42540
CGGGTGCCGG GGAGCGGTCC CCGGCCGGGG CCGCGGTCCC TCTGCCGCGA TCCTTTCTGG 42600
CGAGTCCCCG TGGCCAGTCG GAGAGCGCTC CCTGAGCCGG TCGCGCCCGA GAGGTCGCGC 42660
TGGCCGGCCT TCGGTCCCTC GTGTGTCCCG GTCGTAGGAG GGGCCGGCCG AAAATGCTTC 42720
CGGCTCCCCG TCTGGAGACA CCGGCCGGCC CCTGCGTGTG GCCAGGGCCG CCGGGAGGGC 42780
TCCCCGGCCC GCGCTGTCTC CCGCTGTGTG CCTTGGGTTG ACCAGAGGGA CCCC GGCGC 42840
TCCGTGTGTG GCTGCGATGG TGGCGTTTTT GGGGACAGGT GTCCGTGTCC GTGTCGCGCG 42900
TCGCCTGGGC CGGCGGCGTG GTCGGTGACG CGACCTCCCC GCCCCGGGGG AGGTATATCT 42960
TTCGCTCCGA GTCGGCAATT TTGGGCCGCC GGGTTATAT 42999

```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

CTCCCGCGCG GCCCCCGTGT TCGCCGTTCC CGTGGCGCGG ACAATGCGGT TGTGCGTCCA 60
CGTGTGCGTG TCCGTGCAGT GCCGTTGTGG AGTGCCTCGC TCTCCTCCTC CTCCCGGCA 120
CGGTTCCAC GGTGGGGGAC CACCGGTGAC CTCGCCCTCT TCGGGCCTGG ATCCG 175

```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

GGTCTGGTGG GAATTGTTGA CCTCGCTCTC GGGTGCGGCC TTTGGGGAAC GGC GGGGTCTG 60
GTCGTGCCCG GCGCCGACG TGTGTCGGGG CCCACTTCCC GCTCGAGGGT GGCGGTGGCG 120
GCGGCGTTGG TAGTCTCCCG TGTGCGTCT TCCCGGGCTC TTGGGGGGGG TGCCGTCGTT 180
TTCGGGGCCG GCGTTGCTTG GCTTACGCAG GCTTGGTTTG GGA CTGCCTC AGGAGTCGTG 240
GGCGGTGTGA TTCCCGCCGG TTTTGCTCG CGTCTGCCTG CTTTGCTCG GGT TTGCTTG 300
GTTCGTGTCT CGGGAGCGGT GGT TTTTTTTT TTTTTCGGGT CCCGGGGAGA GGGGTTTTTC 360
CGGGGGACGT TCCCGTCGCC CCCTGCCGCC GGTGGGTTTT CGTTTCGGGC TGTGTTGCTT 420
TCCCCTTCCC CGTTTCGCCG TCGGTTCTCC CCGGTCGGTC GGCCCTCTCC CCGGTCGGTC 480
GCCCCGCCGT GCTGCCGGAC CCCCCCTTCT GGGGGGGATG CCGGGGCACG CACGCGTCCG 540
GGCGGCCACT GTGGTCCGGG AGCTGCTCG CAGGCGGGTG AGCCAGTTGG AGGGGCGTCA 600
TGCCCCCGCG GGCTCCCGTG GCCGACGCGG CGTGTTCTTT GGGGGGGCCT GTGCGTGCGG 660
GAAGGCTGCG CACGTTGTCG GTCCTTGCGA GGGAAAGAGG CTTTTTTTTT TTAGGGGGTC 720
GTCCTTCGTC GTCCGTCGG CGGTGGATCC GGCCT 755

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GGCCGAGGTG | CGTCTGCGGG | TTGGGGCTCG | TCCGGCCCCG | TCGTCCTCCG | GGAAGGCGTT | 60 |
| TAGCGGGTAC | CGTCGCCGCG | CCGAGGTGGG | CGCACGTCGG | TGAGATAACC | CCGAGCGTGT | 120 |
| TTCTGGTTGT | TGGCGGCGGG | GGCTCCGGTC | GATGTCTTCC | CCTCCCCCTC | TCCCCGAGGC | 180 |
| CAGGTCAGCC | TCCGCCTGTG | GGCTTCGTCG | GCCGTCTCCC | CCCCCTCAC | GTCCCTCGCG | 240 |
| AGCGAGCCCG | TCCGTTTCGAC | CTTCCTTCCG | CCTTCCCCCC | ATCTTTCCGC | GCTCCGTTGG | 300 |
| CCCCGGGGTT | TTCACGGCGC | CCCCACGCT | CCTCCGCCTC | TCCGCCCGTG | GTTTGGACGC | 360 |
| CTGGTTCGCG | TCTCCCCGCC | AAACCCCGGT | TGGGTTGGTC | TCCGGCCCCG | GCTTGCTCTT | 420 |
| CGGGTCTCCC | AACCCCGGC | CGGAAGGGTT | CGGGGGTTCC | GGG | | 463 |

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GGATTCTTCA | GGATTGAAAC | CCAAACCGGT | TCAGTTTCCT | TTCCGGCTCC | GGCCGGGGGG | 60 |
| GGCGGCCCCG | GGCGGTTTGG | TGAGTTAGAT | AACCTCGGGC | CGATCGCACG | CCCCCGTG | 120 |
| CGGCGACGAC | CCATTGCAAC | GTCTGCCCTA | TCAACTTTCG | ATGGTAGTCG | ATGTGCCTAC | 180 |
| CATGGTGACC | ACGGGTGACG | GGGAATCAGG | GTTCGATTCC | GGAGAGGGAG | CCTGAGAAAC | 240 |
| GGCTACCACA | TCCAAGGAAG | GCAGCAGGCG | CGCAAATTAC | CCACTCCCGA | CCCGGGGAGG | 300 |
| TAGTGACGAA | AAATAACAAAT | ACAGGACTCT | TTGAGGCCCC | TGTAATTGGA | ATGAGTCCAC | 360 |
| TTTAAATCCT | TTAAGCAG | | | | | 378 |

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| GATCCATTGG | AGGGCAAGTC | TGGTGCCAGC | AGCCGCGGTA | ATTCCAGCTC | CAATAGCGTA | 60 |
| TATTAAAGTT | GCTGCAGTTA | AAAAGCTCGT | AGTTGGATCT | TGGGAGCGGG | CGGGCGGTCC | 120 |
| GCCGCGAGGC | GAGTCAACGC | CCGTCCCCGC | CCCTTGCCCTC | TCGGCGCCCC | CTCGATGCTC | 180 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTAGCTGAGT | TGTCCCGCGG | GGCCCGAAGC | GTTTACTTTG | AAAAAATTAG | AGTTGTTTCA | 240 |
| AAGCAGGCC | GAGCCGCCTG | GATACCGCCA | GCTAGGAAAT | AATGGAATAG | GACCGCGGTT | 300 |
| CCTATTTTGT | TTGGTTTTCG | GAAGTGAGCC | CATGATTAAG | GGAAACGGCC | GGGGGCATTC | 360 |
| CCTTATTGCG | CCCCCCTA | | | | | 378 |

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| GGATCTTTCC | CGCTCCCCGT | TCCTCCCGGC | CCCTCCACCC | GCGCGTCTCC | CCCCTTCTTT | 60 |
| TCCCCTCTCC | GGAGGGGGGG | GAGGTGGGGG | CGCGTGGGCG | GGGTGCGGGG | TGGGGTCGGC | 120 |
| GGGGGACCGC | CCCCGGCCGG | CAAAAGGCCG | CCGCCGGGCG | CACTTCAACC | GTAGCGGTGC | 180 |
| GCCGCGACCG | GCTACGAGAC | GGCTGGGAAG | GCCCGACGGG | GAATGTGGCT | CGGGGGGGGC | 240 |
| GGCGCGTCTC | AGGGCGCGCC | GAACCACTC | ACCCCGAGTG | TTACAGCCCT | CCGGCCGCGC | 300 |
| TTTCGCGGAA | TCCCGGGGCC | GAGGGGAAGC | CCGATACCCG | TCGCCGCGCT | TTTCCCCCTC | 360 |
| CCCCGTCCGC | CTCCCGGGCG | GGCGTGGGGG | TGGGGGCCGG | GCCGCCCCCTC | CCACGCCCGT | 420 |
| GGTTTCTCTC | TCTCCCGGTC | TCGGCCGGTT | TGGGGGGGGG | AGCCCGGTTG | GGGGCGGGGC | 480 |
| GGACTGTCCT | CAGTGCGCC | CGGGCGTCGT | CGCGCCGTCG | GGCCCGGGGG | GTTCTCTCGG | 540 |
| TCACGCCGCC | CCCGACGAAG | CCGAGCGCAC | GGGGTCGGCG | GCGATGTCGG | CTACCCACCC | 600 |
| GACCCGTCTT | GAAACACGGA | CCAAGGAGTC | TAACGCGTGC | GCGAGTCAGG | GGCTCGCACG | 660 |
| AAAGCCGCCG | TGGCGCAATG | AAGGTGAAGG | GCCCCGTCCG | GGGGCCCGAG | GTGGGATCC | 719 |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGAGGCCTCT | CCAGTCCGCC | GAGGGCGCAC | CACCGCCCCG | TCTCGCCCCG | CGCGTCGGGG | 60 |
| AGGTGGAGCA | CGAGCGTACG | CGTTAGGACC | CGAAAGATGG | TGAACTATGC | CTGGGCAGGG | 120 |
| CGAAGCCAGA | GGAAACTCTG | GTGGAGGTCC | GTAGCGGTCC | TGACGTGCAA | ATCGGTCGTC | 180 |
| CGACCTGGGT | ATAGGGGCGA | AAGACTAATC | GAACCATCTA | GTAGCTGGTT | CCCTCCGAAG | 240 |
| TTTCCCTCAG | GATAGCTGGC | GCTCTCGCAA | CCTTCGGAAG | CAGTTTATC | CGGGTAAAGG | 300 |
| CGGAATGGAT | TAGGAGGTCT | TGGGGCCGGA | AACGATCTCA | AACTATTTCT | CAAACTTTAA | 360 |
| ATGGGTAAAG | AAGCCCGGCT | CGCTGGCGTG | GAGCCGGGCG | TGGAATGCGA | GTGCCTAGTG | 420 |
| GGCCACTTTT | GGTAAGCAGA | ACTGGCGCTG | CGGGATGAAC | CGAACGCCGG | GTTAAGGCGC | 480 |
| CCGATGCCGA | CGCTCATCAG | ACCCAGAAA | AGGTGTTGGT | TGATATAGAC | AGCAGGACGG | 540 |
| TGGCCATGGA | AGTCGGAATC | CGCTAAGGAG | TGTGTAACAA | CTCACCTGCC | GAATCAACTA | 600 |
| GCCCTGAAAA | TGGATGGCGC | TGGAGCGTCG | GGCCCATACC | CGGCCGTGCG | CGGCAGTCGG | 660 |
| AACGGGACGG | GACGGGAGCG | GCCGC | | | | 685 |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG

33

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACTGCAGG CCGAGCCACC TCTCTTCTGT GTTTG

35

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGAATTCAC AGAAGAGAGG TGGCTCGGCC TGC

33

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC

34

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAACC CTAACCCTAA CCCTAACCTT AACCTAACCT CTAACCCTAA
CCCTAACCTT AACCCGGGAT

60

80

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGCCCTA GGCTTAAGG

19

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCCAGTCAC GACGT

25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCAAGGC GATTAAGTTG GGTAAC

26

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATGTTGTGT GGAATTGTGA GCGGAT

26

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A

21